

Fri May 24 13:12:20 2002

us-09-784-005-1.ram

Meiler
09/1784005
Seq. ID 1
Page 1

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 105.62 Seconds
(without alignments)
26.660 Million cell updates/sec

Title: US-09-784-005-1

Perfect score: 47
Sequence: 1 DRVYIHPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 3502263 seqs, 351980561 residues

Total number of hits satisfying chosen parameters: 3502263

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Pending_Patents_AA_Main.*

1: /cgn2_6/ptodata/2/paa/US006_COMB.pep.*
2: /cgn2_6/ptodata/2/paa/US006_COMB.pep.*
3: /cgn2_6/ptodata/2/paa/US008_COMB.pep.*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Match Length	ID	Description
1	47	100.0	1 PCT-US00-27741-29	Sequence 29, Appl
2	47	100.0	1 PCT-US01-07479B-2	Sequence 2, Appl
3	47	100.0	1 PCT-US94-10502-1	Sequence 1, Appl
4	47	100.0	1 PCT-US94-10503-1	Sequence 1, Appl
5	47	100.0	1 PCT-US96-16603-3	Sequence 3, Appl
6	47	100.0	1 PCT-US98-15112-2	Sequence 2, Appl
7	47	100.0	8 3 US-07-721-324-2	Sequence 2, Appl

8	47	100.0	3 US-07-791-928-8	Sequence 8, Appl
9	47	100.0	3 US-07-906-396-4	Sequence 4, Appl
10	47	100.0	3 US-07-946-062-21	Sequence 21, Appl
11	47	100.0	4 US-08-085-870-3	Sequence 3, Appl
12	47	100.0	5 US-08-126-368-1	Sequence 1, Appl
13	47	100.0	5 US-08-126-368A-1	Sequence 1, Appl
14	47	100.0	6 US-08-247-451-1	Sequence 1, Appl
15	47	100.0	6 US-08-360-784-4	Sequence 1, Appl
16	47	100.0	7 US-08-360-784-16	Sequence 16, Appl
17	47	100.0	8 US-08-680-004-16	Sequence 1, Appl
18	47	100.0	8 US-08-950-893-1	Sequence 2, Appl
19	47	100.0	8 US-09-022-726-2	Sequence 1, Appl
20	47	100.0	8 US-09-108-478-17	Sequence 17, Appl
21	47	100.0	8 US-09-163-648-17	Sequence 1, Appl
22	47	100.0	8 US-09-198-806-32	Sequence 32, Appl
23	47	100.0	8 US-09-198-806-32	Sequence 32, Appl
24	47	100.0	8 US-09-246-162-1	Sequence 32, Appl
25	47	100.0	8 US-09-246-162-32	Sequence 32, Appl
26	47	100.0	8 US-09-246-162-32	Sequence 32, Appl
27	47	100.0	8 US-09-246-162-32	Sequence 32, Appl
28	47	100.0	8 US-09-250-703-32	Sequence 32, Appl
29	47	100.0	8 US-09-250-703-32	Sequence 32, Appl
30	47	100.0	8 US-09-255-136-1	Sequence 1, Appl
31	47	100.0	8 US-09-255-136-32	Sequence 32, Appl
32	47	100.0	8 US-09-264-563-32	Sequence 32, Appl
33	47	100.0	8 US-09-264-563-32	Sequence 32, Appl
34	47	100.0	8 US-09-266-293A-1	Sequence 1, Appl
35	47	100.0	8 US-09-266-293A-32	Sequence 32, Appl
36	47	100.0	8 US-09-287-674-1	Sequence 1, Appl
37	47	100.0	8 US-09-287-674-32	Sequence 32, Appl
38	47	100.0	8 US-09-297-851-3	Sequence 1, Appl
39	47	100.0	8 US-09-307-940-1	Sequence 32, Appl
40	47	100.0	8 US-09-307-940-32	Sequence 32, Appl
41	47	100.0	8 US-09-332-582-1	Sequence 1, Appl
42	47	100.0	8 US-09-332-582-32	Sequence 32, Appl
43	47	100.0	8 US-09-344-525-1	Sequence 1, Appl
44	47	100.0	8 US-09-413-564-29	Sequence 29, Appl
45	47	100.0	8 US-09-413-564A-24	Sequence 24, Appl

ALIGNMENTS

RESULT 1
PCT-US00-27741-29
Sequence 29, Application PC/TUS0027741
GENERAL INFORMATION:
APPLICANT: The Ohio State University Research Foundation
TITLE OF INVENTION: Antigenic Modification of Polypeptides
FILE REFERENCE: US 2-056 AVPCT
CURRENT APPLICATION NUMBER: PCT/US00/27741
PRIORITY FILING DATE: 2000-10-06
PRIORITY FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 35
SOFTWARE: PatentIn version 3.0
SEQ ID NO 29
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(8)
PCT-US00-27741-29

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 2

PCT-US01-074798-2

Sequence 2, Application PC/TUS01074798

GENERAL INFORMATION:

APPLICANT: Monsanto Company

APPLICANT: GUAN, ZHONGHONG

APPLICANT: TJOENG, FOE SIONG

APPLICANT: LI, WEI

APPLICANT: MANDRELL, KATHY

APPLICANT: LUT, MIN

TITLE OF INVENTION: ANTI-HYPERTENSIVE PEPTIDES

FILE REFERENCE: MTC 6617.1

CURRENT FILING DATE: 2001-03-09

PRIORITY FILING DATE: 2000-03-10

NUMBER OF SEQ ID NOS: 5

SOFTWARE: PatentIn version 3.0

SEQ ID NO 2

LENGTH: 8

TYPE: PRT

ORGANISM: Unknown

FEATURE:

NAME/KEY: PEPTIDE

LOCATION: (1)..(8)

OTHER INFORMATION: Peptide is angiotensin II which is obtained during renin-angioten

PCT-US01-074798-2

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DRYIHPF 8

PCT-US94-10502-1

Sequence 1, Application PC/TUS9410502

GENERAL INFORMATION:

APPLICANT: Rodgers, Kathleen E.

APPLICANT: dizerega, Gere S.

TITLE OF INVENTION: USE OF ANGIOTENSIN II ANALOGS IN TISSUE

NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESS: Robbins, Berliner & Carson

STREET: 201 North Figueroa Street, Fifth Floor

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10502

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Spitals, John P.

REGISTRATION NUMBER: 29,215

REFERENCE/DOCKET NUMBER: 1920-333

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 977-1001

TELEFAX: (213) 977-1003

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US94-10502-1

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DRYIHPF 8

PCT-US94-10503-1

Sequence 1, Application PC/TUS9410503

GENERAL INFORMATION:

APPLICANT: Rodgers, Kathleen E.

APPLICANT: dizerega, Gere S.

TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS

NUMBER OF SEQUENCES: 3

CORRESPONDENCE ADDRESS:

ADDRESS: Robbins, Berliner & Carson

STREET: 201 North Figueroa Street, Fifth Floor

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/10503

FILING DATE:

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Spitals, John P.

REGISTRATION NUMBER: 29,215

REFERENCE/DOCKET NUMBER: 1920-336

TELECOMMUNICATION INFORMATION:

TELEFAX: (213) 977-1001

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

PCT-US94-10503-1

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1 DRYIHPF 8

PCT-US96-16603-3

Sequence 3, Application PC/TUS9616603

GENERAL INFORMATION:

APPLICANT: UNIVERSITY OF MASSACHUSETTS MEDICAL CENTER
TITLE OF INVENTION: PHOTSENSITIVE CAGED MACROMOLECULES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/16603
FILING DATE: 13-OCT-1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/542,927
FILING DATE: 13-OCT-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 04020/055W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
PCT-US96-16603-3

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
|||||
Db 1 DRYIHPF 8

RESULT 6
PCT-US98-15112-2
Sequence 2, Application PC/TUS9815112
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
TITLE OF INVENTION: MULTIPLE TARGET SCREENING OF MOLECULAR
LIBRARIES BY MASS SPECTROMETRY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/15112
FILING DATE: 22-AUG-1998

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,726
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: Anita L. Weikeljohn, Ph.D.
REGISTRATION NUMBER: 35,283
REFERENCE/DOCKET NUMBER: 07334/025W01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US98-15112-2

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
|||||
Db 1 DRYIHPF 8

RESULT 7
US-07-721-324-2
Sequence 2, Application US/07721324
GENERAL INFORMATION:
APPLICANT: Moore, Graham J.
ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: 699 Prince Street
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22313-2404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/721,324
FILING DATE: 19910701
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Dillahunty, T. G.
REGISTRATION NUMBER: 25423
REFERENCE/DOCKET NUMBER: 028722-042
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
TELEX: ITT 440 580 BDSM ALE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-721-324-2

Query Match 100.0%; Score 47; DB 3; Length 8;

Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 8

US-07-791-928-8
Sequence 8, Application US/07791928
GENERAL INFORMATION:

APPLICANT: SHULTZ, JOHN W.
TITLE OF INVENTION: NON-RADIOACTIVE KINASE,
TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCALES, STARK & SAMALL
STREET: 100 E. WISCONSIN AVENUE, SUITE 1100
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version
SOFTWARE: #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/791,928
FILING DATE: 19911112
CLASSIFICATION: 436

ATTORNEY/AGENT INFORMATION:

NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30492
REFERENCE/DOCKET NUMBER: F.3347-1
TELEPHONE: (608) 255-2022
TELEFAX: (608) 255-2182

TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear

MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1

OTHER INFORMATION: /label= LABEL
OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
DETECTION TAG"

US-07-791-928-8

Query Match

Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 9

US-07-906-396-4
Sequence 4, Application US/07906396
GENERAL INFORMATION:

APPLICANT: Harding, J.W.
TITLE OF INVENTION: "Angiotensin IV Peptides and Receptor"
NUMBER OF SEQUENCES: 6

CORRESPONDENCE ADDRESS:

ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
STREET: 2800 Pacific First Center, 1420 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98101-2347

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette-5.25 inch, 1.2mb storage
COMPUTER: IBM PC/386 Compatible
OPERATING SYSTEM: MS-DOS 4.01
SOFTWARE: Word for Windows-t

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/906,396
FILING DATE: 19920624
CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: none
FILING DATE: none
ATTORNEY/AGENT INFORMATION:

NAME: Sundmo, John, S.
REGISTRATION NUMBER: 34,446
REFERENCE/DOCKET NUMBER: WSR-1-6263

TELEPHONE: 1-206-682-8100; 1-206-224-0727 (direct)
TELEFAX: 1-206-224-0779
TELEX: 4938023

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
DESCRIPTION: Angiotensin II
US-07-906-396-4

Query Match

Best Local Similarity 100.0%; Score 47; DB 3; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 10

US-07-946-062-21
Sequence 21, Application US/07946062
GENERAL INFORMATION:

APPLICANT: BODOR, NICHOLAS
TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE
TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis
STREET: George Mason Bldg., Washington & Prince Sts.
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,062
FILING DATE: 17-SEP-1992
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Crane-Feury, Sharon E

REGISTRATION NUMBER: 36,113
 REFERENCE/DOCKET NUMBER: 028724-055
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 836-6620
 TELEFAX: (703) 836-2021
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 1
 OTHER INFORMATION: /note= "Position 1 = H-Asp."
 FEATURE:
 NAME/KEY: Modified-site
 LOCATION: 8
 OTHER INFORMATION: /note= "Position 8 = Phe-OH."
 US-07-946-062-21

Query Match 100.0%; Score 47; DB 3; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 DRVYTHPF 8
 |||||||
 DB 1 DRVYTHPF 8

RESULT 11
 US-08-085-870-3
 Sequence 3, Application US/08085870
 GENERAL INFORMATION:
 APPLICANT: Winn, Martin
 APPLICANT: Zydlowsky, Thomas M.
 APPLICANT: Kerkman, Daniel J.
 APPLICANT: Debernardis, John F.
 APPLICANT: Rosenberg, Saul H.
 APPLICANT: Shiosaki, Kazumi
 APPLICANT: Bashir, Fatima Z.
 APPLICANT: Tasker, Andrew S.
 APPLICANT: von Geldern, Thomas W.
 TITLE OF INVENTION: Angiotensin II Receptor Antagonists
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Edward H. Gorman, Jr.
 STREET: Abbott Laboratories
 STREET: D-377/AP6D
 CITY: Abbott Park
 STATE: Illinois
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 800 KB
 OPERATING SYSTEM: Macintosh IIcx
 SOFTWARE: Microsoft Word 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/085,870
 FILING DATE: 30-JUN-1993
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/844,351
 FILING DATE: 02-MAR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Steven R. Crowley
 REGISTRATION NUMBER: 31,604
 REFERENCE/DOCKET NUMBER: 4840, US.D1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (708) 938-7742
 TELEFAX: (708) 938-2623
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acid residues
 TYPE: amino acid
 TOPOLOGY: unknown
 MOLECULE TYPE:
 DESCRIPTION: peptide
 US-08-085-870-3

Query Match 100.0%; Score 47; DB 4; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 DRVYTHPF 8
 |||||||
 DB 1 DRVYTHPF 8

RESULT 12
 US-08-126-368-1
 Sequence 1, Application US/08126368
 GENERAL INFORMATION:
 APPLICANT: Rodgers, Kathleen E.
 APPLICANT: dizegga, gere S.
 TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS
 TITLE OF INVENTION: THEREOF IN TISSUE REPAIR
 NUMBER OF SEQUENCES: 3
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Robbins, Berliner & Carson
 STREET: 201 North Figueroa Street, Fifth floor
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90012
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/126,368
 FILING DATE:
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: Spitals, John P.
 REGISTRATION NUMBER: 29,215
 REFERENCE/DOCKET NUMBER: 1920-336
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 977-1001
 TELEFAX: (213) 977-1003
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 8 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-126-368-1

Query Match 100.0%; Score 47; DB 5; Length 8;
 Best Local Similarity 100.0%; Pred. No. 3.2e+06; Indels 0; Gaps 0;
 Matches 8; Conservative 0; Mismatches 0;

QY 1 DRVYTHPF 8
 |||||||
 DB 1 DRVYTHPF 8

RESULT 13

US-08-126-368A-1
; Sequence 1, Application US/08126368A
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen E.
; TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS
; TITLE OF INVENTION: THEREOF IN TISSUE REPAIR
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Robbins, Berliner & Carson
; STREET: 201 North Figueroa Street, Fifth Floor
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/126,368A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spitals, John P.
; REGISTRATION NUMBER: 29,215
; REFERENCE/DOCKET NUMBER: 1920-336
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 977-1001
; TELEFAX: (213) 977-1003
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-126-368A-1

Query Match
Best Local Similarity 100.0%; Score 47; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 14
US-08-247-451-1
; Sequence 1, Application US/08247451
; GENERAL INFORMATION:
; APPLICANT: ANANTHANARAYANAN, V. S.
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION AND METHOD
; TITLE OF INVENTION: FOR MEDIATING THE PHYSIOLOGICAL EFFECTS OF A COMPOUND
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Browdy and Neimark
; STREET: 419 Seventh St., Suite 300
; CITY: Washington, N.W.
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/247,451
; FILING DATE:
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/802,982
; FILING DATE: 06-DEC-1991
; APPLICATION NUMBER: US 07/323,421
; FILING DATE: 14-MAR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Cooper, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: ANATHANI
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; TELEX: 248633
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-247-451-1

Query Match
Best Local Similarity 100.0%; Score 47; DB 6; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 15
US-08-360-784-4
; Sequence 4, Application US/08360784
; GENERAL INFORMATION:
; APPLICANT: Harding, J.W.
; TITLE OF INVENTION: Angiotensin IV Peptides and Receptor
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christensen O'Connor Johnson & Kindness
; STREET: 1420 Fifth Ave., Suite 2800
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98101-2347
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,784
; FILING DATE: 22-DEC-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Shelton, Dennis K.
; REGISTRATION NUMBER: 26,997
; REFERENCE/DOCKET NUMBER: MSUR-1-8113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 224-0718
; TELEFAX: (206) 224-0779
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; DESCRIPTION: Angiotensin II
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal

Fri May 24 13:12:20 2002

us-09-784-005-1.rapm

Page 7

ORIGINAL SOURCE:
ORGANISM: Bos taurus
US-08-360-784-4

Query Match 100.0%; Score 47; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 3.2e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
|||||||
Db 1 DRYIHPF 8

Search completed: May 24, 2002, 09:49:32
Job time: 192 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 10.75 Seconds
(without alignments)
21.067 Million cell updates/sec

Title: US-09-784-005-1

Perfect score: 47

Sequence: 1 DRVYIHPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 116914 seqs, 28308587 residues

Total number of hits satisfying chosen parameters: 116914

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

Pending Patents_AA_New:*
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3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*
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6: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*
7: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	8	1 PCT-US02-13383-6	Sequence 6, Appl
2	47	100.0	8	5 US-09-955-780-3	Sequence 3, Appl
3	47	100.0	8	5 US-09-955-780A-3	Sequence 1, Appl
4	47	100.0	8	5 US-09-716-498-1	Sequence 32, Appl
5	47	100.0	8	5 US-09-307-940B-1	Sequence 32, Appl
6	47	100.0	8	5 US-09-307-940B-32	Sequence 7, Appl
7	47	100.0	8	5 US-09-273-597-7	Sequence 1, Appl
8	47	100.0	8	5 US-09-608-532E-1	Sequence 32, Appl
9	47	100.0	8	5 US-09-716-527-1	Sequence 1, Appl
10	47	100.0	8	5 US-09-716-716-1	Sequence 32, Appl
11	47	100.0	8	5 US-09-716-716-32	Sequence 32, Appl
12	47	100.0	8	5 US-10-133-056-6	Sequence 6, Appl
13	47	100.0	8	6 US-10-133-056-6	Sequence 5, Appl
14	47	100.0	10	1 PCT-US02-13383-5	Sequence 37, Appl
15	47	100.0	10	5 US-09-716-498-37	Sequence 37, Appl
16	47	100.0	10	5 US-09-307-940B-37	Sequence 6, Appl
17	47	100.0	10	5 US-09-273-597-6	Sequence 37, Appl
18	47	100.0	10	5 US-09-716-527-37	Sequence 37, Appl
19	47	100.0	10	5 US-09-716-716-37	Sequence 37, Appl
20	47	100.0	10	6 US-10-133-056-5	Sequence 4, Appl
21	47	100.0	10	6 US-09-273-597-4	Sequence 5, Appl
22	47	100.0	12	5 US-09-273-597-5	Sequence 46, Appl
23	47	100.0	13	5 US-09-129-192C-46	Sequence 44, Appl
24	47	100.0	14	6 US-10-115-614-44	Sequence 39, Appl
25	47	100.0	14	6 US-10-138-375-39	
26	47	100.0	14	6 US-10-138-375-39	

27	46	97.9	8	5	US-09-716-498-19	Sequence 19, Appl
28	46	97.9	8	5	US-09-307-940B-19	Sequence 19, Appl
29	46	97.9	8	5	US-09-716-527-19	Sequence 19, Appl
30	46	97.9	8	5	US-09-716-716-19	Sequence 26, Appl
31	45	95.7	8	5	US-09-716-498-26	Sequence 26, Appl
32	45	95.7	8	5	US-09-307-940B-26	Sequence 26, Appl
33	45	95.7	8	5	US-09-716-527-26	Sequence 21, Appl
34	45	95.7	8	5	US-09-716-716-26	Sequence 21, Appl
35	45	95.7	11	5	US-09-307-940B-21	Sequence 21, Appl
36	45	95.7	11	5	US-09-716-527-21	Sequence 21, Appl
37	45	95.7	11	5	US-09-716-716-21	Sequence 23, Appl
38	45	95.7	11	5	US-09-716-498-23	Sequence 23, Appl
39	44	93.6	8	5	US-09-716-498-23	Sequence 23, Appl
40	44	93.6	8	5	US-09-307-940B-23	Sequence 23, Appl
41	44	93.6	8	5	US-09-307-940B-29	Sequence 29, Appl
42	44	93.6	8	5	US-09-716-527-23	Sequence 29, Appl
43	44	93.6	8	5	US-09-716-527-29	Sequence 23, Appl
44	44	93.6	8	5	US-09-716-716-23	Sequence 23, Appl
45	44	93.6	8	5	US-09-716-716-23	Sequence 23, Appl

ALIGNMENTS

RESULT 1
PCT-US02-13383-6
; Sequence 6, Application PC/TUS0213383
; GENERAL INFORMATION:
; APPLICANT: Tanura, Masaaki
; TITLE OF INVENTION: Compositions and Methods of Treating Colorectal Polyps and Can
; FILE REFERENCE: Vanderbilt Ref. No. VU0112; Our Ref. No. 1242-56
; CURRENT APPLICATION NUMBER: PCT/US02/13383
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
; PCT-US02-13383-6

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8

Db 1 DRVYIHPF 8

US-09-955-780-3
; Sequence 3, Application US/09955780
; GENERAL INFORMATION:
; APPLICANT: Kuo, Gee-Hong
; APPLICANT: Connolly, Peter
; APPLICANT: Protay, Catherine
; APPLICANT: DeAngelis, Alan
; APPLICANT: Wang, Aihua
; APPLICANT: Jolliffe, Linda
; APPLICANT: Middleton, Steve
; APPLICANT: Emanuel, Stuart
; TITLE OF INVENTION: Pyrazine Derivatives as Modulators of Tyrosine Kinases
; FILE REFERENCE: ORT-1499
; CURRENT APPLICATION NUMBER: US/09/955,780
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/233,968
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8

;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence:EGF-R substrate
US-09-955-780-3

Query Match
Best Local Similarity 100.0%; Score 47; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 3
US-09-955-780A-3
; Sequence 3, Application US/09955780A
; GENERAL INFORMATION:
; APPLICANT: Kuo, Gee-Hong
; APPLICANT: Connolly, Peter
; APPLICANT: Priouty, Catherine
; APPLICANT: DeAngelis, Alan
; APPLICANT: Wang, Aihua
; APPLICANT: Jolliffe, Linda
; APPLICANT: Middleton, Steve
; TITLE OF INVENTION: Pyrazine Derivatives as Modulators of Tyrosine Kinases
; FILE REFERENCE: ORT-1499
; CURRENT APPLICATION NUMBER: US/09/955,780A
; PRIOR FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: 60/233,968
; PRIOR FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:EGF-R substrate
US-09-955-780A-3

Query Match
Best Local Similarity 100.0%; Score 47; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 4
US-09-716-498-1
; Sequence 1, Application US/09716498
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
; FILE REFERENCE: 9701766
; CURRENT APPLICATION NUMBER: US/09/716,498
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All

US-09-716-498-1

Query Match
Best Local Similarity 100.0%; Score 47; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 5
US-09-716-498-32
; Sequence 32, Application US/09716498
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Method for Promoting Hematopoietic and Mesenchymal Cell
; FILE REFERENCE: 9701766
; CURRENT APPLICATION NUMBER: US/09/716,498
; PRIOR FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 14
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: PHOSPHORYLATION
US-09-716-498-32

Query Match
Best Local Similarity 100.0%; Score 47; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 6
US-09-307-940B-1
; Sequence 1, Application US/09307940B
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dizerega, Gere
; TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After
; FILE REFERENCE: 9701761
; CURRENT APPLICATION NUMBER: US/09/307,940B
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All

Query Match
Best Local Similarity 100.0%; Score 47; DB 5; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8

Db 1 DRYIHPF 8

RESULT 7
US-09-307-940B-32
; Sequence 32, Application US/09307940B
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzerega, Gere
; TITLE OF INVENTION: Methods to Increase White Blood Cell Survival After
; TITLE OF INVENTION: Chemotherapy
; FILE REFERENCE: 97017P1
; CURRENT APPLICATION NUMBER: US/09/307,940B
; CURRENT FILING DATE: 1999-05-10
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All analogue 14
; NAME/KEY: MOD_RES
; LOCATION: (4)
; OTHER INFORMATION: PHOSPHORYLATION
US-09-307-940B-32

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
1 DRYIHPF 8

RESULT 8
US-09-273-597-7
; Sequence 7, Application US/09273597
; GENERAL INFORMATION:
; APPLICANT: Verdine, Greg L.
; APPLICANT: Chytil, Milan
; APPLICANT: Malinky, Tiffany
; APPLICANT: Diduk, Mary T.
; TITLE OF INVENTION: SYNTHESIS OF COMPOUNDS AND LIBRARIES OF
; TITLE OF INVENTION: COMPOUNDS
; FILE REFERENCE: 00246-258001
; CURRENT APPLICATION NUMBER: US/09/273,597
; CURRENT FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 60/079,035
; PRIOR FILING DATE: 1998-03-23
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-273-597-7

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
1 DRYIHPF 8

RESULT 9
US-09-608-532E-1

; Sequence 1, Application US/09608532E
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzerega, Gere
; TITLE OF INVENTION: Use of Angiotensin II Fragments and Analogs Thereof in Tissue
; FILE REFERENCE: USC010.1CP2CCP (00-1188-E)
; CURRENT APPLICATION NUMBER: US/09/608,532E
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION:
; OTHER INFORMATION: synthetic peptide
US-09-608-532E-1

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
1 DRYIHPF 8

RESULT 10
US-09-716-527-1
; Sequence 1, Application US/09716527
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K4
; CURRENT APPLICATION NUMBER: US/09/716,527
; CURRENT FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:All
US-09-716-527-1

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
1 DRYIHPF 8

RESULT 11
US-09-716-527-32
; Sequence 32, Application US/09716527
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen
; APPLICANT: dzerega, Gere
; TITLE OF INVENTION: Radiation Therapy Methods
; FILE REFERENCE: 97017K4
; CURRENT APPLICATION NUMBER: US/09/716,527
; CURRENT FILING DATE: 2000-11-20
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 32

LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All analogue 14
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: PHOSPHORYLATION
US-09-716-527-32

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 12
US-09-716-716-1
Sequence 1, Application US/09716716
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
TITLE OF INVENTION: Radiation Therapy Methods
FILE REFERENCE: 97017K5
CURRENT APPLICATION NUMBER: US/09/716,716
CURRENT FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 1
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All
US-09-716-716-1

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 13
US-09-716-716-32
Sequence 32, Application US/09716716
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
TITLE OF INVENTION: Radiation Therapy Methods
FILE REFERENCE: 97017K5
CURRENT APPLICATION NUMBER: US/09/716,716
CURRENT FILING DATE: 2000-11-20
NUMBER OF SEQ ID NOS: 38
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 32
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: All analogue 14
NAME/KEY: MOD_RES
LOCATION: (4)
OTHER INFORMATION: PHOSPHORYLATION

US-09-716-716-32

Query Match 100.0%; Score 47; DB 5; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 14
US-10-133-056-6
Sequence 6, Application US/10133056
GENERAL INFORMATION:
APPLICANT: Tamura, Masaaki
TITLE OF INVENTION: Compositions and Methods of Treating Colorectal Polyps and Can
FILE REFERENCE: Vanderbilt Ref. No. VU0112; Our Ref. No. 1242-56
CURRENT APPLICATION NUMBER: US/10/133,056
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln version 3.1
SEQ ID NO 6
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-133-056-6

Query Match 100.0%; Score 47; DB 6; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

RESULT 15
PCT-US02-13383-5
Sequence 5, Application PC/TUS0213383
GENERAL INFORMATION:
APPLICANT: Tamura, Masaaki
TITLE OF INVENTION: Compositions and Methods of Treating Colorectal Polyps and Can
FILE REFERENCE: Vanderbilt Ref. No. VU0112; Our Ref. No. 1242-56
CURRENT APPLICATION NUMBER: PCT/US02/13383
CURRENT FILING DATE: 2002-04-26
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentln version 3.1
SEQ ID NO 5
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
PCT-US02-13383-5

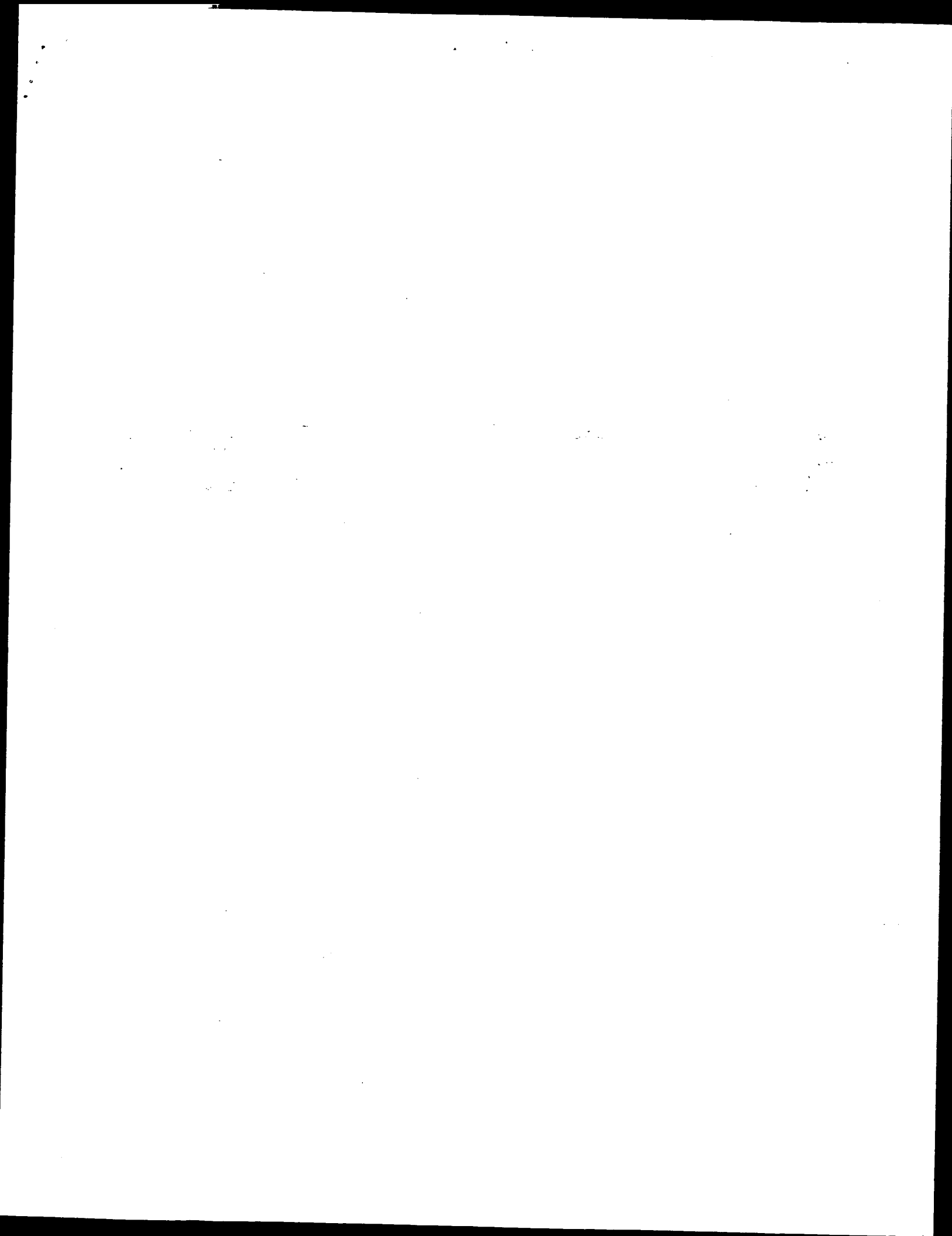
Query Match 100.0%; Score 47; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
|||||||
Db 1 DRVYIHPF 8

Search completed: May 24, 2002, 09:49:49
Too time: 209 sec

Fri May 24 13:12:20 2002

us-09-784-005-1.rapn



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OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 29.95 seconds
(without alignments)
29,669 Million cell updates/sec

Title: US-09-784-005-1

Perfect score: 47

Sequence: 1 DRVYIHPF 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_032802.*
1: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT.*
2: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT.*
3: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT.*
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6: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT.*
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12: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT.*
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14: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT.*
15: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT.*
16: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT.*
17: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT.*
18: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT.*
19: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT.*
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21: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT.*
22: /SIDSL/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	6	AA050467
2	47	100.0	8	11	AA07584
3	47	100.0	8	14	AA07433
4	47	100.0	8	16	AA083013
5	47	100.0	8	16	AA084269
6	47	100.0	8	17	AA05193
7	47	100.0	8	17	AA095662
8	47	100.0	8	18	AA033309
9	47	100.0	8	18	AA032951
10	47	100.0	8	18	AA011201
11	47	100.0	8	18	AA014975

12	47	100.0	8	18	AA09656
13	47	100.0	8	18	AA019144
14	47	100.0	8	19	AA065596
15	47	100.0	8	19	AA064758
16	47	100.0	8	19	AA064728
17	47	100.0	8	19	AA065628
18	47	100.0	8	19	AA071141
19	47	100.0	8	19	AA065538
20	47	100.0	8	19	AA059280
21	47	100.0	8	19	AA045523
22	47	100.0	8	19	AA049586
23	47	100.0	8	20	AA0495614
24	47	100.0	8	20	AA039917
25	47	100.0	8	20	AA033901
26	47	100.0	8	20	AA042367
27	47	100.0	8	20	AA030539
28	47	100.0	8	20	AA030568
29	47	100.0	8	20	AA030583
30	47	100.0	8	20	AA030612
31	47	100.0	8	20	AA032750
32	47	100.0	8	20	AA032743
33	47	100.0	8	20	AA033797
34	47	100.0	8	20	AA033768
35	47	100.0	8	20	AA015373
36	47	100.0	8	20	AA015340
37	47	100.0	8	20	AA015345
38	47	100.0	8	20	AA015333
39	47	100.0	8	20	AA021824
40	47	100.0	8	20	AA094002
41	47	100.0	8	21	AA027397
42	47	100.0	8	21	AA027401
43	47	100.0	8	21	AA027432
44	47	100.0	8	21	AA028130
45	47	100.0	8	21	AA028130

ALIGNMENTS

RESULT 1
ID AAP50467 standard; peptide: 8 AA.
XX AAP50467;
AC
DT 01-DEC-1991 (first entry)
DE
Sequence of cyclopropyl peptide with anti-hypertensive activity.
KW Cyclopropyl peptide; analgetic; CNS regulator;
KW blood pressure regulator; renin inhibitor; anti-hypertensive;
KW bradykinin inhibitor; shock therapy.
XX
XX W08500809-A.
XX
XX 28-FEB-1985.
XX
XX 14-AUG-1984; 84WO-US01278.
XX
XX 03-AUG-1984; 84US-0636091.
XX 16-AUG-1983; 83US-0523808.
XX 15-DEC-1988; 88US-0285542.
XX
XX (UYGE-) UNIV OF GEORGIA RES.
XX
XX Stammer CH;
XX
XX WPI; 1985-062273/10.
XX
XX New cyclopropyl-amino acids and peptide(s) - useful as
XX therapeutic agents, sweetening agents etc.
XX
XX Example; Table II, Page 24; 82pp; English.
PS

Labelled peptide s
Isoelectric point
Angiotensin II, H
Angiotensin II pep
Angiotensin II oct
Angiotensin II
Angiotensin II ana
Angiotensin II pep
Angiotensin II, H
Homo sapiens angio
Angiotensin II, H
Angiotensin II oct
Angiotensin analog
Human angiotensin
Angiotensin II oct
Angiotensin II ana
Angiotensin II sequenc
Amino acid sequenc
Amino acid sequenc
Amino acid sequenc
Angiotensin II pep
Angiotensin II ana
Angiotensin II (AI
Angiotensin II (AI
Angiotensin II (AI
Angiotensin II (AI
Angiotensin II pe
Angiotensin II pep
Angiotensin II oct
Angiotensinogen II
Angiotensin II ana
Angiotensin II ana

XX When used to replace normal AAs in a peptide chain, the cyclopropyl
 CC AAs stabilise the peptide against enzymatic cleavage and acid
 CC hydrolysis, and the peptide has good long term stability. Peptides
 CC as bicyclic AAs have numerous pharmacological properties, e.g.
 CC as bacteriostats, antihypertensives, analgesics, CNS regulators, blood
 CC pressure regulators, renin inhibitors, antihypertensives and
 CC bradykinin inhibitors for shock treatment. They may also be
 CC herbicides, pesticides etc. Dose is 50-100 mg/kg for intravascular
 CC admin. in AAs0467, optionally the following AAs are cyclopropyl
 CC residues: 1,2,3,4,6,8, 4 and 8, 4 and 6, 6 and 8.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 6; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 1 drvylhpf 8

RESULT 2
 AAR07584
 ID AAR07584 standard; protein; 8 AA.
 XX
 AC AAR07584;
 XX
 DT 08-FEB-1991 (first entry)
 XX
 DE Hypotensive polypeptide.
 XX
 KW Gamma-casein.
 XX
 OS Zea mays.
 XX
 PN JP02240027-A.
 XX
 PD 25-SEP-1990.
 XX
 PF 14-MAR-1989; 89JP-0059549.
 XX
 PR 14-MAR-1989; 89JP-0059549.
 XX
 PA (AGEN) AGENCY OF IND SCI TECH.
 XX
 PA (SHOS) SHOWA KK.
 XX
 DR WPI; 1990-332335/44.
 XX
 PT New polypeptide hypotensive agents - are tri-, penta- or
 PT hexapeptide(s) derived from gamma casein
 XX
 PS Claim 1; Page 193; 5pp; Japanese.
 XX
 CC Peptide, derived from Zea mays gamma-casein, is useful as an anti-
 CC hypotensive agent in mammals and humans.
 CC
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 11; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 1 drvylhpf 8

RESULT 3
 AAR37433

ID AAR37433 standard; peptide; 8 AA.
 XX
 AC AAR37433;
 XX
 DT 08-SEP-1993 (first entry)
 XX
 DE Promega peptide 8.
 XX
 KW Modified peptide substrate; non-radioactive; detection; dansyl;
 KW sulphorhodamine 101; lissamine; rhodamine; enzymes; phosphatases;
 KW protein kinases; proteases.
 XX
 OS Synthetic.
 XX
 FT Key Location/Qualifiers
 FT Modified-site 1
 FT /note- "detection tag- lissamine, Rhodamine"
 XX
 PN W09310461-A.
 XX
 PD 27-MAY-1993.
 XX
 PF 12-NOV-1992; 92WO-US09595.
 XX
 PR 12-NOV-1991; 91US-0791928.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Shultz JW, White DH;
 DR WPI; 1993-182698/22.
 XX
 PT Quantitating presence or activity of enzyme - by incubating with
 PT modified peptide substrate and measuring the modified peptide
 PT prod.
 XX
 PS Claim 24; Page 27; 103pp; English.
 XX
 CC Promega peptide 4 is tagged with dansyl at residue 1 and may be used
 CC in a novel non-radioactive method of quantitating the presence or
 CC activity of an enzyme. The method can be used for rapid, specific
 CC and highly sensitive detection of enzymes such as protein kinases,
 CC phosphatases and proteases, esp. in this case for tyrosine kinase.
 CC They can be used to study enzyme function in metabolism and in
 CC diagnosis of disease. They also allow quantitative determ. of the
 CC enzyme's activity. See also AAR37426-36.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 14; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 1 drvylhpf 8

RESULT 4
 AAR83013
 ID AAR83013 standard; peptide; 8 AA.
 XX
 AC AAR83013;
 XX
 DT 11-APR-1996 (first entry)
 XX
 DE Promega protein kinase substrate peptide G.
 XX
 KW Promega; peptide; substrate; G; protein kinase; activity; assay.
 XX
 OS Synthetic.
 XX

PN WO9523612-A1.
 XX
 PD 08-SEP-1995.
 XX
 PF 06-MAR-1995; 95WO-US02856.
 XX
 PR 04-MAR-1994; 94US-0208573.
 XX
 PA (PROM-) PROMEGA CORP.
 XX
 PI Goueli SA;
 XX
 DR WPI; 1995-320414/41.
 XX
 PT Quantitating activity of a selected protein kinase on a peptide
 XX substrate - by conjugating the substrate to a binding cpd.
 PS
 XX Claim 15; Page 35; 49pp; English.
 XX
 CC The activity of a selected protein kinase (PK), pref. Ser-Thr or
 CC Tyr PK, is quantified by conjugating a binding cpd to a peptide
 CC substrate, pref. one of the Promega peptides A-H (AAR83007-14), adding
 CC this to a PK contg. soln., incubating the soln. to form a modified
 CC peptide prod. and then measuring the activity of the PK.
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYIHFP 8
 |||||
 Db 1 dryyihpf 8

RESULT 5

AAR84269
 ID AAR84269 standard; peptide; 8 AA.
 XX

AC AAR84269;
 XX

DT 11-APR-1996 (first entry)
 XX

DE Angiotensin II decomposition peptide useful as a hypotensive agent.
 XX

XX Angiotensin: hypertension; inhibition; hypotensive functional food;
 KW ACE; angiotensin converting enzyme.
 XX

OS Synthetic.
 XX

PN JP07215889-A.
 XX

PD 15-AUG-1995.
 XX

PF 27-JAN-1994; 94JP-0023615.
 XX

PR 27-JAN-1994; 94JP-0023615.
 XX

PA (SENMI-) SENMI EKESU KK.
 XX

DR WPI; 1995-317421/41.
 XX

XX Hypotensive agent and functional food - composed of angiotensin II
 PT decomposition peptide
 XX

PS Claim 1; Page 2; 6pp; Japanese.
 XX

CC AAR84268 and AAR84269 are angiotensin II-derived decomposition peptides.
 CC They are useful as hypotensive agents and may be used in a
 CC hypotensive functional food. The peptides show excellent ACE
 CC inhibiting activity and can be used as effective hypotensive agents.

XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 16; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYIHFP 8
 |||||
 Db 1 dryyihpf 8

RESULT 6

AAR65193
 ID AAR65193 standard; peptide; 8 AA.
 XX

AC AAR65193;
 XX

DT 02-OCT-1998 (first entry)
 XX

DE Angiotensin II.
 XX

KW Bradykinin; N-benzylglycine; agonist; receptor study; antagonist;
 KW achiral; analgesic; angiotensin II.
 XX

OS Synthetic.
 XX

PN US5527882-A.
 XX

PD 18-JUN-1996.
 XX

PF 07-NOV-1994; 94US-0335202.
 XX

PR 07-JUL-1989; 89US-0376839.
 XX

PR 16-SEP-1992; 92US-0945664.
 XX

PR 07-NOV-1994; 94US-0335202.
 XX

PA (REGC) UNIV CALIFORNIA.
 XX

PI Mitchell AR, Young JD;
 XX

DR WPI; 1996-299898/30.
 XX

XX New bradykinin analogues contg. N-benzyl-L-glycine - useful as
 PT bradykinin agonists or antagonists, useful e.g. as analgesics
 XX

PS Disclosure; Columns 9-10; 15pp; English.
 XX

CC The invention relates to the obtaining of a potent agonist or antagonist
 CC peptide by the replacement of selected amino acids with synthetic
 CC achiral amino acids. The present sequence represents angiotensin II
 CC in which such an amino acid change can be made.
 XX

SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYIHFP 8
 |||||
 Db 1 dryyihpf 8

RESULT 7

AAR95662
 ID AAR95662 standard; peptide; 8 AA.
 XX

AC AAR95662;
 XX

DT 09-JAN-1997 (first entry)

XX Angiotensin II.
 XX
 KW Angiotensin II; AT2; vasoconstrictor; arteriole; angiotensin; renin;
 KW angiotensinogen; angiotensinase; wound repair; tissue growth; skin; burn;
 KW ulcer; periodontal disease; intraperitoneal surgical wound; hypertensive.
 XX
 OS Synthetic.
 XX
 PN WO9614858-A1.
 XX
 PD 23-MAY-1996.
 XX
 XX 14-NOV-1995; 95MO-US14764.
 PF
 XX 06-JUN-1995; 95US-0465775.
 PR 14-NOV-1994; 94US-0337781.
 XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX
 PI Dizerega GS, Rodgers K;
 XX
 DR WPI; 1996-259561/26.
 XX
 PT Accelerating wound healing by application of angiotensin II
 PT fragments - are effective at very low concn. and do not cause
 PT hypertension
 XX
 PS Disclosure; Page 2; 46pp; English.
 XX
 CC This sequence represents angiotensin II (AT2). AT2 is an octapeptide
 CC present in humans and other species. AT2 is one of the most potent
 CC vasoconstrictors known, causing constriction of the arterioles. The
 CC formation of angiotensin is initiated by the action of renin on
 CC angiotensinogen. The substance formed is a decapeptide called
 CC angiotensin I which is converted by the enzyme angiotensinase (by
 CC removal of the C-terminal His-Leu) into AT2. AT2 increases the release
 CC of extracellular matrices involved in wound repair. Fragments of this
 CC sequence (see AAR95663-R95672) can be used in a compound for
 CC accelerating wound healing. The compounds are administered for
 CC or micellar solutions, formulated with a carrier or diluent,
 CC alternatively the compound is applied in conjunction with a wound
 CC dressing. The carrier used in the composition is preferably
 CC carboxymethylcellulose, crystalloids, viscoelastic, or poly glycols. By
 CC using fragments of this sequence (or analogues of it), growth as well as
 CC healing of tissues is improved, such as in cases of wounds on the skin
 CC (e.g. ulcers, burns, periodontal disease, cuts) or intraperitoneal
 CC surgical wounds. The compounds containing the AT2 fragments are less
 CC hypertensive than full length AT2, and are also effective at much lower
 CC (nanomolar) concentrations than full length AT2.
 CC
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 17; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DRVYIHPF 8
 DB 1 drvylhpf 8
 XX
 RESULT 8
 AAMW33309 standard; peptide: 8 AA.
 XX
 AC AAMW33309;
 XX
 DT 05-FEB-1998 (first entry)
 XX
 DE Targeting conjugate for bis-nicotinamide bifunctional chelator.
 XX

KW Bifunctional; bis-nicotinamide; chelator; radioactive; technetium;
 KW rhodium; conjugate; endothelin; angiotensin; targeting agent;
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
 KW delivery.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9710853-A2.
 XX
 PD 27-MAR-1997.
 XX
 XX 19-SEP-1996; 96MO-DE01824.
 PF
 XX 21-SEP-1995; 95DE-4036783.
 PR
 XX
 PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 XX
 PI Dinkelborg L, Hilger CS, Kramp W, Platzek J;
 PI Raduechel B;
 XX
 DR WPI; 1997-212562/19.
 XX
 XX New bis-nicotinamide bi-functional chelating agents - forming new,
 PT stable technetium or rhodium complexes and conjugates useful as
 PT radio diagnostic and radio-therapeutic agents
 XX
 PS Claim 11; Page 42; 47pp; German.
 XX
 CC Novel bis-nicotinamide bifunctional chelating agent for radioactive
 CC technetium and rhodium, when conjugated to an endothelin or
 CC angiotensin derived targeting agent, e.g. the present peptide, can
 CC be used for the in vivo imaging of organs, receptors and receptor
 CC containing tissues and/or atherosclerotic plaques, e.g. for the
 CC diagnosis of breast or prostatic carcinoma. They can also be used
 CC for cytostatic agent delivery.
 CC
 XX
 SQ Sequence 8 AA;
 XX
 Query Match 100.0%; Score 47; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 DRVYIHPF 8
 DB 1 drvylhpf 8
 XX
 RESULT 9
 AAMW32951 standard; peptide: 8 AA.
 XX
 AC AAMW32951;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Targeting conjugate for bifunctional sulphonamide type ligand.
 XX
 KW Bifunctional sulphonamide; ligand; radioactive; technetium;
 KW rhodium; conjugate; endothelin; angiotensin; targeting agent;
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
 KW delivery.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN DE19536785-A1.
 XX
 PD 27-MAR-1997.
 XX

PF 21-SEP-1995; 95DE-1036785.
 XX
 PR 21-SEP-1995; 95DE-1036785.
 XX
 PA (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 XX
 PI Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 XX Raduechel B;
 XX WPI; 1997-193894/18.
 DR
 XX Bifunctional sulphonomide type ligands for radioactive technetium or
 PT rhenium - and their chelates and conjugates, useful for imaging
 PT carcinoma or atherosclerosis
 PS
 XX Claim 9; Page 11; 12pp; German.
 CC Novel bifunctional sulphonomide type ligands for radioactive
 CC technetium and rhenium, when conjugated to an endothelin or
 CC angiotensin derived targeting agent, e.g. the present peptide, can
 CC be used for the in vivo imaging of organs, receptors and receptor
 CC containing tissues and/or atherosclerotic plaques, e.g. for the
 CC diagnosis of breast or prostatic carcinoma. They can also be used
 CC for cytostatic agent delivery.
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 Db 1 dryvlyhpf 8
 RESULT 10
 AAW11201
 ID AAW11201 standard; peptide: 8 AA.
 XX
 AC AAW11201;
 XX
 DT 26-JAN-1998 (first entry)
 XX
 DE Targeting conjugate for bifunctional sulphonomide type ligand.
 XX
 KW Bifunctional sulphonomide; ligand; radioactive; technetium;
 KW rhenium; conjugate; endothelin; angiotensin; targeting agent;
 KW organ; in vivo imaging; receptor; tissue; atherosclerotic plaque;
 KW diagnosis; breast; prostatic; carcinoma; cytostatic agent;
 KW delivery.
 XX
 XX Homo sapiens.
 OS Synthetic.
 OS
 XX DE19356780-A1.
 PN
 XX
 PD 27-MAR-1997.
 PS
 XX 21-SEP-1995; 95DE-1036780.
 PF
 XX 21-SEP-1995; 95DE-1036780.
 PR
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 PI Raduechel B;
 PI WPI; 1997-193892/18.
 DR
 XX Bifunctional sulphonomide type ligands for radioactive technetium
 PT and rhenium - and their chelates and conjugates with targeting

PT agents, useful for imaging carcinoma, atherosclerotic plaque, etc.
 XX
 XX Claim 11; Page 18; 19pp; German.
 PS
 XX Novel bifunctional sulphonomide type ligands for radioactive
 CC technetium and rhenium, when conjugated to an endothelin or
 CC angiotensin derived targeting agent, e.g. the present peptide, can
 CC be used for the in vivo imaging of organs, receptors and receptor
 CC containing tissues and/or atherosclerotic plaques, e.g. for the
 CC diagnosis of breast or prostatic carcinoma. They can also be used
 CC for cytostatic agent delivery.
 CC
 XX
 SQ Sequence 8 AA;
 Query Match 100.0%; Score 47; DB 18; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 Db 1 dryvlyhpf 8
 RESULT 11
 AAW14975
 ID AAW14975 standard; peptide: 8 AA.
 XX
 AC AAW14975;
 XX
 DT 28-NOV-1997 (first entry)
 XX
 DE Conjugating peptide for radio-therapeutic/diagnostic agent.
 XX
 KW Conjugate; diseased tissue; endothelin; angiotensin; chemotactic;
 KW radiodiagnostic; radiotherapeutic; diagnosis; tumour; ischaemia;
 KW atherosclerosis; vascular disorder; ischemia.
 XX
 XX Synthetic.
 OS
 OS WO9710852-A2.
 PN
 XX
 PD 27-MAR-1997.
 PS
 XX 19-SEP-1996; 96WO-DE01821.
 PF
 XX 21-SEP-1995; 95DE-4036781.
 PR
 XX (UYBE-) UNIV BERLIN INST DIAGNOSTIKFORSCHUNG.
 PA
 XX Dinkelborg L, Erber S, Hilger CS, Kramp W, Platzek J;
 PI Raduechel B;
 PI WPI; 1997-202627/18.
 DR
 XX New sulphide-sulphonamide bi:functional chelating agents - forming
 PT new, stable technetium or rhenium complexes and conjugates useful as
 PT radiodiagnostic and radio-therapeutic agents
 PT
 XX Claim 13; Page 44; 50pp; German.
 PS
 XX XSNS-type bifunctional sulphide containing sulphonomide chelating
 CC agents and their technetium or rhenium complexes, can form
 CC covalently bonded conjugates with substances selectively enriched
 CC in diseased tissue, e.g. the present peptide. The substance is an
 CC endothelin or angiotensin peptide, or a partial sequence, analogue,
 CC derivative or antagonist, or a chemotactic peptide.
 CC The conjugates are radiodiagnostic or radiotherapeutic agents,
 CC useful in the diagnosis of tumours, ischaemia or atherosclerotic
 CC vascular disorders.
 CC
 XX
 SQ Sequence 8 AA;

Query Match 100.0%; Score 47; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 dryvlyhpf 8

RESULT 12

AAW09656
ID AAW09656 standard; peptide; 8 AA.

AC AAW09656;

DT 20-MAY-1997 (first entry)

DE Labelled peptide substrate used in enzyme activity assay.

KW Enzyme activity; assay; measurement; label; rhodamine; dansyl;
KM non-radioactive; electrophoretic separation; protein kinase; protease;
phosphatase.

OS Synthetic.

PH Key Location/Qualifiers

FT Modified-site 1 /note= "labelled with rhodamine B detection tag"

PN US5580747-A.

PD 03-DEC-1996.

PF 12-NOV-1991; 91US-0791928.

PR 21-JAN-1994; 94US-0185448.

PR 12-NOV-1991; 91US-0791928.

PA (PROM-) PROMEGA CORP.

PI Shultz JW, White DH;

DR WPI; 1997-033568/03.

PT Non-radioactive assay for measuring enzyme activity - involving
PT electrophoretic sepn. of labelled cleavage prod. from labelled
PT peptide substrate

PS Claim 5; Column 41-42; 35pp; English.

AAW09656 is a peptide substrate used in a non-radioactive assay for
measuring enzyme activity. The assay comprises incubating the enzyme
with the labelled peptide substrate to form a labelled peptide
product; separating the product from the substrate by agarose gel
electrophoresis and measuring the amount of product by detecting the
label by fluorescence or chemiluminescence. The assay can be
performed rapidly and with great sensitivity. This peptide is
especially for determining tyrosine kinase activity, e.g. to study
its function in metabolism or to screen for potential inhibitors.

Sequence 8 AA;

Query Match

Best Local Similarity 100.0%; Score 47; DB 18; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 dryvlyhpf 8

RESULT 13

AAW19144
ID AAW19144 standard; peptide; 8 AA.

AC AAW19144;

DT 06-AUG-1997 (first entry)

DE Isoelectric point marker peptide 4 based on angiotensin I.

KW Label; fluorescent dye; isoelectric; point; PI; marker; focusing;
KM fluorescence; capillary; stable; angiotensin I.

OS Synthetic.

PN EP744614-A2.

PD 27-NOV-1996.

PF 29-MAR-1996; 96EP-0105113.

PR 19-OCT-1995; 95JP-0271196.

PR 31-MAR-1995; 95JP-0076873.

PA (MOLE-) LAB MOLECULAR BIOPHOTONICS.

PI Kasal K, Matsumoto H, Shimura K, Takamoto H;

DR WPI; 1997-001360/01.

PT Isoelectric point markers for isoelectric focusing - comprising
PT fluorescence-labelled oligo:nucleotide(s)

PS Claim 6; Page 21; 29pp; English.

The present peptide, when labelled with a fluorescent dye, can be
used as an isoelectric point (PI) marker for isoelectric focusing
with fluorescence. The dye is linked to the peptide's
amino-terminal through an amide, thioamide, sulphonamide, urea,
thiourea or urethane bond, and is rhodamine, fluorescein, cyanine,
indocyanine, indocarbocyanine, pyronine, lucifer yellow,
quinacrine, squarillium, coumarin, fluoroanthranil maleimide or
anthracene. The marker can be used for capillary isoelectric
focusing, and it is possible to construct peptide sets that cover
a wide PI range and have good storage stability.
The present peptide has respective observed and calculated PI
values of 5.30 and 5.20.

Sequence 8 AA;

Query Match 100.0%; Score 47; DB 18; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.4e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 dryvlyhpf 8

RESULT 14

AAW65596
ID AAW65596 standard; peptide; 8 AA.

AC AAW65596;

DT 09-NOV-1998 (first entry)

DE Angiotensin II.

KW angiotensin II; skin graft; AII analogue; tissue repair; vasoconstrictor;
KM wound healing.

XX

OS Homo sapiens.
 XX XX
 PN WO9826795-A1.
 XX XX
 PD 25-JUN-1998.
 XX XX
 PF 16-DEC-1997; 97WO-US23461.
 XX XX
 PR 15-DEC-1997; 97US-0990664.
 PR 16-DEC-1996; 96US-0028310.
 XX XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX XX
 PI Dizerega GS, Rodgers KE;
 XX XX
 DR WPI; 1998-362518/31.
 XX XX
 PT Promoting incorporation of skin graft onto underlying tissue -
 PT comprises pre-treating graft with angiotensin II, or analogue or
 PT peptide fragment
 XX XX
 PS Claim 1; Page 1; 82pp; English.
 XX XX
 CC The invention relates to the use of angiotensin II (AII), AII analogues,
 CC AII fragments and AII fragment analogues for promoting incorporation of a
 CC skin graft into underlying tissue of a mammal. The peptides are effective
 CC in accelerating the growth or healing of skin grafts and in accelerating
 CC re-epithelialisation and tissue repair, even at very low concentrations.
 CC They can significantly accelerate the rate of healing at nanomolar levels
 CC in vivo. AII accelerates wound repair by increased neovascularisation,
 CC growth factor release, re-epithelialisation, extracellular matrix production
 CC and increased flow of blood and nutrients to the injured tissue. Use of
 CC the above peptides other than AII itself (an extremely potent vaso-
 CC constrictor) may avoid the side-effects of AII, such as increase in blood
 CC pressure and thirst. The present sequence represents angiotensin II.
 CC XX
 SQ Sequence 8 AA:
 OY 1 DRVYIHPF 8
 Db 1 drvylhpf 8
 Query Match 100.0%; Score 47; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 RESULT 15
 AAW64758
 ID AAW64758 standard; peptide; 8 AA.
 AC XX
 XX AAW64758;
 DT XX
 XX 02-NOV-1998 (first entry)
 DE Angiotensin II peptide analogue 14.
 XX XX
 KW Proliferation; mesenchymal stem cell; lineage-specific cell;
 KW haematopoietic; cell culture; transplantation; treatment; malignant;
 KW inherited disease; angiotensinogen; angiotensin I; angiotensin II.
 XX XX
 OS Synthetic.
 OS Homo sapiens.
 OS XX
 FH Key Location/Qualifiers
 FT Modified-site 4 /note="Modified by (P03)2 group"
 XX XX
 PN WO9832457-A2.
 XX XX
 PD 30-JUL-1998.
 XX XX

PF 26-JAN-1998; 98WO-US01552.
 XX XX
 PR 23-JAN-1998; 98US-0066593.
 PR 28-JAN-1997; 97US-0036507.
 PR 08-MAY-1997; 97US-0046859.
 PR 28-OCT-1997; 97US-0063684.
 PR 31-OCT-1997; 97US-0063910.
 PR 18-NOV-1997; 97US-0065612.
 PR 26-NOV-1997; 97US-0066593.
 XX XX
 PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
 XX XX
 PI dizerega G, Rodgers KE;
 XX XX
 DR WPI; 1998-437044/37.
 XX XX
 PT Promoting haematopoietic and mesenchymal cell proliferation and
 PT differentiation - by contacting the cells with angiotensinogen,
 PT angiotensin I or II, or analogues or fragments of these
 XX XX
 PS Disclosure; Page 18; 114pp; English.
 XX XX
 CC AAW64728-W64763 are peptides used in a novel method for accelerating the
 CC proliferation of mesenchymal stem cells (MSCs), haematopoietic
 CC lineage-specific cells or mesenchymal lineage-specific cells. The method
 CC involves contacting the cells with an active agent comprising a sequence
 CC consisting of at least three contiguous amino acids of groups R1-R8 in
 CC the sequence of formula, R1-R2-R3-R4-R5-R6-R7-R8. R1 and R2 together
 CC form a group of formula X-Ra-Rb-, X = H or a 1-3 peptide group, R3 = Val,
 CC Ala, Leu, norleu, Ile, Gly, Pro, Alb, Acpc (1-aminocyclopentane
 CC carboxylic acid) or Tyr, R4 = Tyr, Tyr(P03)2, Thr, Ser, homoser or
 CC azatyrl, R5 = Ile, Ala, Leu, norleu, Val or Gly; R6 = His, Arg or
 CC 6-NH2-Phe, R7 = Pro or Ala, R8 = Phe, Phe(Br), Ile or Tyr, Ra and Rb are
 CC not defined in the specification, the peptide bond between Ra and Rb is
 CC labile to aminopeptidase A cleavage excluding sequences including R4 as a
 CC terminal Tyr group. A second active agent comprising a sequence
 CC consisting of at least three contiguous amino acids of groups R2-R8, in
 CC the sequence of formula R2-R3-R4-R5-R6-R7-R8 where R2 = H, Arg, Lys, Ala,
 CC Orn, Ser(Ac), Sar, D-Arg or D-Lys; R3, R4, R5, R6, R7, R8 is also
 CC described. The inventions are particularly useful in cell culture
 CC mediums. These cells may be used in transplantation techniques for
 CC treatment of malignant or inherited diseases. The formulae represent
 CC analogues of angiotensinogen, angiotensin I (AII), angiotensin II (AII),
 CC or AII AT2 type 2 receptor agonists.
 CC XX
 SQ Sequence 8 AA:
 OY 1 DRVYIHPF 8
 Db 1 drvylhpf 8
 Query Match 100.0%; Score 47; DB 19; Length 8;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 24, 2002, 09:47:40
 Job time: 80 sec

Fri May 24 13:12:16 2002

us-09-784-005-1.rag

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 13.03 Seconds
(without alignments)
14.997 Million cell updates/sec

Title: US-09-784-005-1

Sequence: 1 DRYIHPF 8

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
2: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/prodata/2/1aa/5A.COMB.pep:*
4: /cgn2_6/prodata/2/1aa/5B.COMB.pep:*
5: /cgn2_6/prodata/2/1aa/PTUS.COMB.pep:*
6: /cgn2_6/prodata/2/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	8	1	US-07-858-842-2
2	47	100.0	8	1	US-08-021-839A-3
3	47	100.0	8	1	US-08-184-935-2
4	47	100.0	8	1	US-08-212-433A-29
5	47	100.0	8	1	US-08-185-448-8
6	47	100.0	8	1	US-07-776-272-1
7	47	100.0	8	1	US-08-428-488-21
8	47	100.0	8	1	US-08-337-781-1
9	47	100.0	8	1	US-08-240-711-20
10	47	100.0	8	1	US-08-594-117-1
11	47	100.0	8	1	US-08-520-770-2
12	47	100.0	8	1	US-08-457-753-20
13	47	100.0	8	2	US-08-115-968-1
14	47	100.0	8	2	US-08-465-774-1
15	47	100.0	8	2	US-08-360-784B-2
16	47	100.0	8	2	US-08-623-833B-4
17	47	100.0	8	2	US-08-465-775-1
18	47	100.0	8	2	US-08-542-927-3
19	47	100.0	8	3	US-08-716-256-29
20	47	100.0	8	3	US-09-054-308A-2
21	47	100.0	8	3	US-09-280-047-7
22	47	100.0	8	3	US-09-208-337-1
23	47	100.0	8	3	US-08-990-664-1
24	47	100.0	8	3	US-08-927-128-16
25	47	100.0	8	4	US-09-210-249-1
26	47	100.0	8	4	US-09-373-962-1
27	47	100.0	8	4	US-09-373-962-32

28	47	100.0	8	4	US-09-289-693-25	Sequence 25, Appl
29	47	100.0	8	4	US-09-245-680-1	Sequence 1, Appl
30	47	100.0	8	4	US-09-245-680-32	Sequence 32, Appl
31	47	100.0	8	4	US-09-198-806C-1	Sequence 1, Appl
32	47	100.0	8	4	US-09-198-806C-32	Sequence 32, Appl
33	47	100.0	8	4	US-09-352-191-1	Sequence 1, Appl
34	47	100.0	8	4	US-09-352-191-32	Sequence 32, Appl
35	47	100.0	8	4	US-09-300-434-1	Sequence 1, Appl
36	47	100.0	8	4	US-09-012-400-32	Sequence 32, Appl
37	47	100.0	8	4	US-08-208-573B-7	Sequence 1, Appl
38	47	100.0	8	4	US-08-10258-1	Sequence 32, Appl
39	47	100.0	8	5	PCT-US95-02856-7	Sequence 7, Appl
40	47	100.0	8	5	PCT-US95-03239-29	Sequence 29, Appl
41	47	100.0	8	6	5169865-1	Sequence 1, Appl
42	47	100.0	8	6	5451571-3	Sequence 1, Appl
43	47	100.0	8	6	5459077-1	Sequence 1, Appl
44	47	100.0	9	2	US-08-360-784B-13	Sequence 13, Appl
45	47	100.0	9	2		

ALIGNMENTS

RESULT 1
US-07-858-842-2
Sequence 2, Application US/07858842
Patent No. 5314807
GENERAL INFORMATION:
APPLICANT: Yoshikawa, Masaaki
APPLICANT: Yokoyama, Keiichi
APPLICANT: Hasegawa, Masayasu
APPLICANT: Yasumoto, Ryouichi
APPLICANT: Fujita, Hiroyuki
TITLE OF INVENTION: METHOD FOR PRODUCING AN ANGIOTENSIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESSES:
ADDRESSEE: ARMSTRONG & KUBOVIC
ADDRESS: 1725 K Street N.W. Suite 1000
CITY: Washington
STATE: District of Columbia
COUNTRY: United States of America
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/858,842
FILING DATE: 19920327
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 142283
FILING DATE: 29-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 298060
FILING DATE: 17-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 34,409
REFERENCE/DOCKET NUMBER: 920247
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 659-2930
TELEFAX: (202) 887-0357
TELEX: 440142
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: N-terminal

ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-07-858-842-2

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 2

US-08-021-839A-3
Sequence 3, Application US/08021839A
Patent No. 5326776

GENERAL INFORMATION:

APPLICANT: Wind, Martin
APPLICANT: De, Bismarck
APPLICANT: Zydney, Thomas M.
APPLICANT: Kerkman, Daniel J.
APPLICANT: Debernardis, John F.
APPLICANT: Rosenberg, Saul H.
APPLICANT: Shlosaki, Kazumi
APPLICANT: Basna, Fatima Z.
APPLICANT: Spina, Kenneth P.
TITLE OF INVENTION: Angiotensin II Receptor Antagonists
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman, Jr.
STREET: Abbott Laboratories
STREET: D-377/AP6D
STREET: One Abbott Park Road
CITY: Abbott Park
STATE: Illinois
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 800 KB
COMPUTER: Apple Macintosh Ixci
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021.839A
FILING DATE: 24-FEB-1993
CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/844,817
FILING DATE: 02-MAR-1992

ATTORNEY/AGENT INFORMATION:

NAME: Steven R. Crowley

REGISTRATION NUMBER: 31,604

REFERENCE/DOCKET NUMBER: 5136 US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (708) 938-7742

TELEFAX: (708) 938-2623

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acid residues

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-021-839A-3

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 3

US-08-184-935-2
Sequence 2, Application US/08184935
Patent No. 5476770

GENERAL INFORMATION:

APPLICANT: PRADILES, PHILIPPE

TITLE OF INVENTION: IMMUNOMETRIC DETERMINATION OF AN ANTIGEN

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,

STREET: 1755 S. Jefferson Davis Highway, Suite 400

CITY: Arlington

STATE: Virginia

COUNTRY: U.S.A.

ZIP: 22202

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/184,935

FILING DATE: 24-JAN-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Oblon, No. 5476770man F.

REGISTRATION NUMBER: 24,618

REFERENCE/DOCKET NUMBER: 846-286-0

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 413-3000

TELEFAX: (703) 413-2220

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: unknown

MOLECULE TYPE: peptide

US-08-184-935-2

Query Match
Best Local Similarity 100.0%; Score 47; DB 1; Length 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 4

US-08-212-433A-29
Sequence 29, Application US/08212433A
Patent No. 5538897

GENERAL INFORMATION:

APPLICANT: Yates, III, John R.

TITLE OF INVENTION: USE OF MASS SPECTROMETRY FRAGMENTATION

NUMBER OF SEQUENCES: 46

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend Kourie and Crew

STREET: One Market Plaza, Steuart St. Tower

CITY: San Francisco

STATE: CA

COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/212,433A
FILING DATE: 14-MAR-1994
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Hughes, Richard L.
REGISTRATION NUMBER: 31,264
REFERENCE/DOCKET NUMBER: 16336-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-212-433A-29

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYIHPF 8
|||||||
DB 1 DRVYIHPF 8

RESULT 5
US-08-185-448-8
Sequence 8, Application US/08185448
Patent No. 5580747
GENERAL INFORMATION:
APPLICANT: SHULTZ, JOHN W.
TITLE OF INVENTION: NON-RADIOACTIVE KINASE,
TITLE OF INVENTION: PHOSPHATASE AND PROTEASE ASSAY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: ANDRUS, SCALES, STARKE & SAWALL
STREET: 100 E. WISCONSIN AVENUE, SUITE 1100
CITY: MILWAUKEE
STATE: WISCONSIN
COUNTRY: USA
ZIP: 53202
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version
SOFTWARE: #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/185,448
FILING DATE: 21-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/791,928
FILING DATE: 12-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: SARA, CHARLES S
REGISTRATION NUMBER: 30492
REFERENCE/DOCKET NUMBER: F.3347-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 255-2022

TELEFAX: (608) 255-2182
TELEX: 26832 ANDSTARK
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1
OTHER INFORMATION: /label= LABEL
OTHER INFORMATION: /note= "LOCATION OF LISSAMINE RHODAMINE
OTHER INFORMATION: DETECTION TAG"
US-08-185-448-8

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYIHPF 8
|||||||
DB 1 DRVYIHPF 8

RESULT 6
US-07-776-272-1
Sequence 1, Application US/07776272
Patent No. 5612454
GENERAL INFORMATION:
APPLICANT: Kaminuma, Yoshihiko
APPLICANT: Iida, Toshi
TITLE OF INVENTION: Process for Purification of Polypeptide
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wegner, Cantor, Mueller & Player
STREET: 1233 20th St. N.W. P.O. Box 18218
CITY: Washington
STATE: District of Columbia
COUNTRY: United States of America
ZIP: 20036-8218
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/776,272
FILING DATE: 19911129
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Player, William E
REGISTRATION NUMBER: 31,409
REFERENCE/DOCKET NUMBER: P-450-23167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-887-0400
TELEFAX: 202-887-0605
TELEX: 440706
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-07-776-272-1

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
Db 1 DRYIHPF 8

RESULT 7

US-08-428-488-21
; Sequence 21, Application US/08428488
; Patent No. 5624894

GENERAL INFORMATION:

APPLICANT: BODOR, Nicholas S.

TITLE OF INVENTION: BRAIN-ENHANCED DELIVERY OF NEUROACTIVE

TITLE OF INVENTION: PEPTIDES BY SEQUENTIAL METABOLISM

NUMBER OF SEQUENCES: 107

CORRESPONDENCE ADDRESS:

ADDRESSEE: Burns, Doane, Swecker & Mathis

STREET: P.O. Box 1404

CITY: Alexandria

STATE: Virginia

COUNTRY: United States

ZIP: 22313-1404

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/428,488

FILING DATE: 27-APR-1995

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Baumeister, Mary Katherine

REGISTRATION NUMBER: 26, 254

REFERENCE/DOCKET NUMBER: 028724-087

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620

TELEFAX: (703) 836-6620

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 1

OTHER INFORMATION: /note="Position 1 = H-asp."

NAME/KEY: Modified-site

LOCATION: 8

OTHER INFORMATION: /note="Position 8 = Phe-OH."

US-08-428-488-21

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8

Db 1 DRYIHPF 8

RESULT 8

US-08-337-781-1
; Sequence 1, Application US/08337781
; Patent No. 5629292
; GENERAL INFORMATION:
; APPLICANT: Rodgers, Kathleen E.
; APPLICANT: dizerega, Gere S.
; TITLE OF INVENTION: USE OF ANGIOTENSIN III AND ANALOGS

TITLE OF INVENTION: THEROF IN TISSUE REPAIR
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:

ADDRESSEE: Robbins, Berliner & Carson

STREET: 201 No. 5629292th Figueroa Street, Fifth floor

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90012

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/337,781

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Spitals, John P.

REGISTRATION NUMBER: 29, 215

REFERENCE/DOCKET NUMBER: 1920-336C

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 977-1001

TELEFAX: (213) 977-1003

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-337-781-1

Query Match

Best Local Similarity 100.0%; Score 47; DB 1; Length 8;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8

Db 1 DRYIHPF 8

RESULT 9

US-08-240-711-20

; Sequence 20, Application US/08240711

; Patent No. 5679777

GENERAL INFORMATION:

APPLICANT: ANDERSON, DAVID C.

APPLICANT: MATHEWS, ANTHONY J.

TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/240,711

FILING DATE: 12-JUL-1994

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US92/09713

FILING DATE: 06-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/789,177

FILING DATE: 08-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,179
FILING DATE: 08-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON=5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-240-711-20

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 10
US-08-594-117-1
Sequence 1, Application US/08594117
Patent No. 5716935
GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen E.
APPLICANT: dilerega, Gere S.
TITLE OF INVENTION: USE OF ANGIOTENSIN II ANALOGS IN TISSUE
TITLE OF INVENTION: REPAIR
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Robbins, Berliner & Carson
STREET: 201 No. 5716935th Figueroa Street, Fifth Floor
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,117
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/126,370
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Spitals, John P.
REGISTRATION NUMBER: 29,215
REFERENCE/DOCKET NUMBER: 1920-333
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 977-1001
TELEFAX: (213) 977-1003
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-594-117-1

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 11
US-08-520-770-2
Sequence 2, Application US/08520770
Patent No. 5723307
GENERAL INFORMATION:
APPLICANT: Tsai, Hsin
APPLICANT: Chen, Hui-Liang
TITLE OF INVENTION: Fluorogenic Substrates for Assay of
TITLE OF INVENTION: Angiotensin Converting Enzyme
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores LLP
STREET: 4370 La Jolla Village Drive, Suite 700
City: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/520,770
FILING DATE: 30-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LI 1791
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-520-770-2

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
DB 1 DRYIHPF 8

RESULT 12
US-08-457-753-20
Sequence 20, Application US/08457753
Patent No. 5759512
GENERAL INFORMATION:
APPLICANT: ANDERSON, DAVID C.
APPLICANT: MATHEWS, ANTHONY J.
TITLE OF INVENTION: HEMOGLOBINS AS DRUG DELIVERY AGENTS
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:

ADDRESSEE: Browdy and Neimark
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,753
FILING DATE: 01-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/240,711
FILING DATE: 12-JUL-1994
APPLICATION NUMBER: PCT/US92/09713
FILING DATE: 06-NOV-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,177
FILING DATE: 08-NOV-1991
APPLICATION NUMBER: US 07/789,179
FILING DATE: 08-NOV-1991

ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
REFERENCE/DOCKET NUMBER: ANDERSON=5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-457-753-20

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 13
US-08-115-968-1
Sequence 1, Application US/08115968
Patent No. 5824696

GENERAL INFORMATION:
APPLICANT: Griswold E, Don
TITLE OF INVENTION: Medicaments
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham
STREET: P. O. Box 1539
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406-0939

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/115,968
FILING DATE: 01-SEP-1993
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Dinner, Dara L
REGISTRATION NUMBER: 33,680
REFERENCE/DOCKET NUMBER: P50192
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610) 270-5017
TELEFAX: (610) 270-5090

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-115-968-1

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 14
US-08-465-774-1
Sequence 1, Application US/08465774
Patent No. 5834432

GENERAL INFORMATION:
APPLICANT: Rodgers, Kathleen
TITLE OF INVENTION: USE OF ANGIOGENSIN II TYPE
TITLE OF INVENTION: 2 RECEPTOR AGONISTS IN TISSUE REPAIR
NUMBER OF SEQUENCES: 2

CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobb, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
CITY: Newport Beach
STATE: CA
COUNTRY: U.S.A.
ZIP: 92660

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,774
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER: USC011,001A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
TELEFAX: 714-760-9502
TELEX:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-774-1

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

Db 1 DRYIHPF 8

Search completed: May 24, 2002, 09:46:43
Job time: 23 sec

OY 1 DRYIHPF 8
Db 1 DRYIHPF 8

RESULT 15
US-08-360-784B-2
Sequence 2, Application US/08360784B
Patent No. 5854388
GENERAL INFORMATION:
APPLICANT: Harding, J.W.
APPLICANT: Wright, J.W.
TITLE OF INVENTION: Angiotensin IV Peptides and Receptor
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Christensen O'Connor Johnson & Kindness
STREET: 1420 Fifth Ave., Suite 2800
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101-2347
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,784B
FILING DATE: 22-DEC-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Shelness, Diana K.
REGISTRATION NUMBER: 35,356
REFERENCE/DOCKET NUMBER: WSR-1-8113
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 224-0735
TELEFAX: (206) 224-0779
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: Angiotensin II
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
ORGANISM: Bos taurus
FEATURE:
NAME/KEY: Modified-site
LOCATION: Multiple
OTHER INFORMATION:
OTHER INFORMATION: /note= Includes variants from which deletions have been made
OTHER INFORMATION: at the C-terminus by 1, 2, 3, 4, or 5 residues.
US-08-360-784B-2

Query Match 100.0%; Score 47; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.7e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0;

OY 1 DRYIHPF 8

Fri May 24 13:12:19 2002

us-09-784-005-1.rai

Page 8

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:20 ; Search time 14.71 Seconds
(without alignments)
52.258 Million cell updates/sec

Title: US-09-784-005-1

Perfect score: 47

Sequence: 1 DRVYIHPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: PIR_71:*
2: PIR1:*
3: PIR2:*
4: PIR3:*
5: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	47	100.0	10	S65432	angiotensin I - ho
2	47	100.0	14	A01250	angiotensin precur
3	47	100.0	15	A60834	angiotensin I prec
4	47	100.0	476	JC2318	angiotensin precu
5	47	100.0	477	ANRT	angiotensin precu
6	47	100.0	477	A29978	angiotensin precu
7	47	100.0	485	1 ANHU	angiotensin I - Ja
8	46	97.9	10	A06624	angiotensin I - Ja
9	46	97.9	10	A06917	angiotensin precu
10	46	97.9	10	A03045	angiotensin precu
11	45	95.7	11	S07207	Clinia-angiotensin
12	41	87.2	540	S72233	transcription fact
13	40	85.1	128	G81220	hypothetical prote
14	40	85.1	132	F82800	thrombin (EC 3.4.2
15	37	78.7	625	1 TBBO	hypothetical prote
16	36	76.6	277	2 E86229	hypothetical prote
17	36	76.6	289	2 C96610	hypothetical prote
18	35	74.5	167	2 AE2630	hypothetical prote
19	35	74.5	305	2 D69362	tRNA intron endom
20	35	74.5	1355	1 VGBE11	149K glycoprotein
21	34	72.3	183	2 B95125	acetyltransferase,
22	34	72.3	185	2 F97995	conserved hypotet
23	34	72.3	316	2 T34838	probable transfera
24	34	72.3	360	1 DMBY1H	L-serine dehydrata
25	34	72.3	481	2 S76115	hypothetical prote
26	34	72.3	510	2 E84094	2,3-bisphosphoglyc
27	34	72.3	525	2 G83173	GMP synthase PA376
28	34	72.3	736	2 D86271	protein F16A14.2 l
29	34	72.3	1224	2 T07446	DNA-directed RNA p

30	34	72.3	3165	2 S15010	hypothetical prote
31	33	70.2	56	2 H82647	hypothetical prote
32	33	70.2	178	2 B42845	3-hydroxybutyrate
33	33	70.2	221	2 A86163	protein F15K5.22 l
34	33	70.2	329	2 S28305	hypothetical prote
35	33	70.2	332	1 A44509	UDPglucose 4-epime
36	33	70.2	333	2 JC5313	UDPglucose 4-epime
37	33	70.2	416	2 AF2070	hypothetical prote
38	33	70.2	422	2 A69644	threonine dehydrat
39	33	70.2	510	2 A56142	phosphoglycerate m
40	33	70.2	559	2 A12227	hypothetical prote
41	33	70.2	617	2 S10511	thrombin (EC 3.4.2
42	33	70.2	622	1 TBHU	thrombin (EC 3.4.2
43	33	70.2	681	2 I78558	hypothetical Brach
44	33	70.2	695	1 S05008	complement subcomp
45	33	70.2	695	2 T24950	hypothetical prote

ALIGNMENTS

RESULT 1
S65432
angiotensin I - horn fly (fragment)
C:Species: Haematobia irritans (horn fly)
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C:Accession: S65432
R:Wiljfelds, G.; Fitzgerald, C.; Gough, J.; Ridding, G.; Elvin, C.; Kemp, D.; Willadsen
Eur J. Biochem. 237, 414-423, 1996
A>Title: Cloning and characterisation of angiotensin-converting enzyme from the dipte
A:Reference number: S65431; MUID:96215437
A:Accession: S65432
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <MID>
A>Note: the source is designated as Haematobia irritans exigu

Query Match 100.0%; Score 47; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.0043;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 2
A01250
angiotensin precursor - horse (fragment)
C:Species: Equus caballus (domestic horse)
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Mar-1998
C:Accession: A92775; A01250
R:Skoggs Jr., L.T.; Kahn, J.R.; Lentz, K.; Shumway, N.P.
J. Exp. Med. 106, 439-453, 1957
A:Reference number: A92775
A:Accession: A92775
A:Molecule type: protein
A:Residues: 1-14 <SKE>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; hormone; vasoconstrictor
F:1-10/Product: angiotensin I #status experimental <ANI>
F:1-8/Product: angiotensin II #status experimental <ANI>

Query Match 100.0%; Score 47; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.0061;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DB 1 DRVYIHPF 8

RESULT 3
A:Accession: A60834
N:Contains: angiotensin I precursor - dog (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C:Accession: A93945, A90456, A01251
R:Okubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A:Title: Cloning and sequene analysis of cDNA for rat angiotensinogen.
A:Reference number: A93945; MUID:83169849
A:Accession: A93945
A:Molecule type: mRNA
A:Residues: 1-477 <OK>
A:Cross-references: GB:J00704; NID:9202912; PID:AAA98779.1; PID:9202914
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A:Title: Rat angiotensinogen and Des(angiotensin)angiotensinogen: purification, char
A:Reference number: A90456; MUID:82091819
A:Accession: A90456
A:Molecule type: protein
A:Residues: 25-41 <BOU>
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MP>
F:25-34/Product: angiotensin II #status experimental <PP>
F:25-32/Product: angiotensin III #status experimental <PP2>
F:26-32/Product: angiotensin III #status experimental <PP3>
F:295-319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 47; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.0066;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYTHPF 8
DB 1 DRYTHPF 8

RESULT 4
JC2318
angiotensin precursor - sheep
N:Alternate names: angiotensinogen
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C:Accession: JC2318; A25406
R:Manase, M.; Suzuki, F.; Fukumizu, A.; Takeda, N.; Takeuchi, K.; Murakami, K.; Nakamura
Biosci. Biotechnol. Biochem. 58, 1884-1885, 1994
A:Title: Sequencing and expression of sheep angiotensinogen cDNA.
A:Reference number: JC2318; MUID:95072318
A:Accession: JC2318
A:Molecule type: mRNA
A:Residues: 1-476 <NAG>
A:Cross-references: DDBJ:DJ7520; NID:9575593; PIDN:BA04470.1; PID:g1197183
A:Experimental source: liver
A:Note: the authors translated the codon TTC for residue 465 as Leu
R:Pernley, R.T.; John, M.; Niall, H.D.; Coghlan, J.P.
Eur. J. Biochem. 154, 597-601, 1986
A:Title: Purification and characterization of ovine angiotensinogen.
A:Reference number: A25406; MUID:86136099
A:Accession: A25406
A:Molecule type: protein
A:Residues: 25-37, 'X', '39 <FER>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:24-476/Product: angiotensinogen #status predicted <MP>
F:25-34/Product: angiotensin #status predicted <MP2>
F:295-362/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 47; DB 1; Length 476;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYTHPF 8
DB 25 DRYTHPF 32

RESULT 5
ANRT

angiotensin precursor - rat
N:Contains: angiotensin I; angiotensin II; angiotensin III
C:Species: Rattus norvegicus (Norway rat)
C:Date: 13-Jun-1983 #sequence_revision 13-Jun-1983 #text_change 18-Jun-1999
C:Accession: A93945, A90456, A01251
R:Okubo, H.; Kageyama, R.; Ujihara, M.; Hirose, T.; Inayama, S.; Nakanishi, S.
Proc. Natl. Acad. Sci. U.S.A. 80, 2196-2200, 1983
A:Title: Cloning and sequene analysis of cDNA for rat angiotensinogen.
A:Reference number: A93945; MUID:83169849
A:Accession: A93945
A:Molecule type: mRNA
A:Residues: 1-477 <OK>
A:Cross-references: GB:J00704; NID:9202912; PID:AAA98779.1; PID:9202914
R:Bouhnik, J.; Clauser, E.; Strosberg, D.; Frenoy, J.P.; Menard, J.; Corvol, P.
Biochemistry 20, 7010-7015, 1981
A:Title: Rat angiotensinogen and Des(angiotensin)angiotensinogen: purification, char
A:Reference number: A90456; MUID:82091819
A:Accession: A90456
A:Molecule type: protein
A:Residues: 25-41 <BOU>
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs.
C:Comment: The release of the amino-terminal residue (Asp-25) from angiotensin I and
sp-1]angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
ung.
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MP>
F:25-34/Product: angiotensin II #status experimental <PP>
F:25-32/Product: angiotensin III #status experimental <PP2>
F:26-32/Product: angiotensin III #status experimental <PP3>
F:295-319/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 47; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYTHPF 8
DB 25 DRYTHPF 32

RESULT 6
A29978
angiotensin precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A29978
R:Clouston, W.M.; Evans, B.A.; Haralambidis, J.; Richards, R.I.
Genomics 2, 240-248, 1988
A:Title: Molecular cloning of the mouse angiotensinogen gene.
A:Reference number: A29978; MUID:86284703
A:Accession: A29978
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-477 <CLO>
A:Cross-references: GB:AF045887; GB:J03046; NID:92842773; PIDN:AAC01765.1; PID:928427
C:Genetics:
A:Introns: 277/1; 366/2; 414/3
C:Superfamily: antithrombin III
C:Keywords: blood pressure control
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-477/Product: angiotensinogen #status predicted <MP>

Query Match 100.0%; Score 47; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.28;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYTHPF 8

DB 25 DRVYTHPF 32

RESULT 7

ANHU
angiotensin precursor [validated] - human
N:Alternate names: angiotensinogen
N:Contains: angiotensin I; angiotensin II; angiotensin III
C:Species: Homo sapiens (man)
C:Date: 06-Jul-1982 #sequence_revision 19-Jan-1996 #text_change 08-Dec-2000
C:Accession: A33203; A31362; I37169; A60825; I39462; A90487; A90226; I54281; A01
R:Fukamizu, A.; Takahashi, S.; Seo, M.S.; Tada, M.; Tanimoto, K.; Uehara, S.; Murakami,
J. Biol. Chem. 265, 7576-7582, 1990
A:Title: Structure and expression of the human angiotensinogen gene. Identification of a
A:Reference number: A35203; MUID:90237063
A:Accession: A35203
A:Molecule type: DNA
A:Residues: 1-485 <FUK>
A:Cross-references: GB:X15323; GB:X15324; GB:X15325; GB:X15326; GB:X15327
R:Galliard, I.; Clauser, E.; Corvol, P.
DNA 8, 87-99, 1989
A:Title: Structure of human angiotensinogen gene.
A:Reference number: A31362; MUID:89170129
A:Accession: A31362
A:Molecule type: DNA
A:Residues: 1-267, 'M', 269-332, 'E', 334-485 <GAT>
A:Cross-references: GB:M24686; GB:M24687; GB:M24688
A:Note: The authors translated the codon GAA for residue 333 as Gln
R:Nibu, Y.; Takahashi, S.; Tanimoto, K.; Murakami, K.; Fukamizu, A.
J. Biol. Chem. 269, 28598-28605, 1994
A:Title: Identification of cell type-dependent enhancer core element located in the 3'-c
A:Reference number: I37168; MUID:95050659
A:Accession: I37168
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-285 <NIB>
A:Cross-references: EMBL:X15324; NID:g1197496; PIDN:CMA33385.1; PID:g1197497
A:Accession: I37169
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 287-375 <NIB>
A:Cross-references: EMBL:X15325; NID:g28695
R:Kunapuli, S.P.; Benedict, C.R.; Kumar, A.
Arch. Biochem. Biophys. 254, 642-646, 1987
A:Title: Tissue specific hormonal regulation of the rat angiotensinogen gene expression.
A:Reference number: A60825; MUID:87212053
A:Accession: A60825
A:Molecule type: mRNA
A:Residues: 32-184 <KUN>
R:Kunapuli, S.P.; Kumar, A.
Circ. Res. 60, 786-790, 1987
A:Title: Molecular cloning of human angiotensinogen cDNA and evidence for the presence of
A:Reference number: I39462; MUID:87244745
A:Accession: I39462
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-267, 'M', 269-338 <KUN>
A:Cross-references: GB:M69110; NID:g178643; PIDN:AAA52282.1; PID:g553181
R:Kageyama, R.; Ohkubo, H.; Nakamishi, S.
Biochemistry 23, 3603-3609, 1984
A:Title: Primary structure of human preangiotensinogen deduced from the cloned cDNA sequ
A:Reference number: A90487; MUID:85000455
A:Accession: A90487
A:Molecule type: mRNA
A:Residues: 1-267, 'M', 269-485 <KAG>
A:Cross-references: GB:K02215; NID:g178639; PIDN:AAA51731.1; PID:g178640
A:Note: It is uncertain whether Met-1 or Met-10 is the initiator
R:Tewksbury, D.A.; Dart, R.A.; Travis, J.
Biochem. Biophys. Res. Commun. 99, 1311-1315, 1981
A:Title: The amino terminal amino acid sequence of human angiotensinogen.
A:Reference number: A90226; MUID:81255848
A:Accession: A90226

A:Molecule type: protein
A:Residues: 34-46, 'X', 48-50, 'S', 52-57, 'D' <TEW>
R:Hixson, J.E.; Powers, P.K.
Hum. Genet. 96, 110-112, 1995
A:Title: Detection and characterization of new mutations in the human angiotensinogen
A:Reference number: I54281; MUID:95331754
A:Accession: I54281
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 176-241, 'I', 243-267, 'M', 269-287, 'ANLSAG' <HIX>
A:Cross-references: GB:S78529; NID:g999316; PIDN:AD14287.1; PID:g4261987
C:Comment: Angiotensin I is released from angiotensinogen by renin, which is secreted
e I (angiotensin-converting enzyme), primarily in the lungs
C:Comment: The release of the amino-terminal residue (Asp-34) from angiotensin I and
sp-1 angiotensin I is converted to angiotensin III by dipeptidyl carboxypeptidase I.
C:Comment: Angiotensin II causes vasoconstriction by direct action on blood vessels,
o induces thirst.
C:Comment: Angiotensin II and angiotensin III are equally potent in stimulating the s
C:Comment: Angiotensinogen is synthesized in the liver and secreted into the plasma.
C:Genetics:
A:Gene: GDB:AGT
A:Cross-references: GDB:118750; OMIM:106150
A:Map position: 1942-1943
A:Introns: 286/1; 375/2; 423/3
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor
F:1-33/Domain: (or 10-33) signal sequence #status predicted <SIG>
F:34-485/Product: angiotensinogen #status predicted <MPT>
F:34-43/Product: angiotensin I #status experimental <PP1>
F:34-41/Product: angiotensin II #status experimental <PP2>
F:34-41/Product: angiotensin III #status experimental <PP3>
F:47,170,304,328/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 47; DB 1; Length 485;
Best Local Similarity 100.0%; Pred. No. 0.29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYTHPF 8
Db 34 DRVYTHPF 41

RESULT 8
A60624
angiotensin I - Japanese quail
C:Species: Coturnix coturnix japonica (Japanese quail)
C:Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 07-May-1999
C:Accession: A60624
R:Takel, Y.; Hasegawa, Y.
Gen. Comp. Endocrinol. 79, 12-22, 1990
A:Title: Vasopressor and depressor effects of native angiotensins and inhibition of t
A:Reference number: A60624; MUID:90284684
A:Accession: A60624
A:Molecule type: protein
A:Residues: 1-10 <TAK>
C:Superfamily: antithrombin III
C:Keywords: blood pressure control; glycoprotein; liver; plasma; vasoconstrictor

Query Match 97.9%; Score 46; DB 2; Length 10;
Best Local Similarity 87.5%; Pred. No. 0.0066;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYTHPF 8
Db 1 DRVYTHPF 8

RESULT 9
A90917
angiotensin precursor - chicken (fragment)
C:Species: Gallus gallus (chicken)

C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
 C:Accession: A90917; A01250
 R:Nakayama, T.; Nakajima, T.; Sökabe, H.
 Chem. Pharm. Bull. 21: 2085-2087, 1973
 A>Title: Comparative studies on angiotensins. III. Structure of fowl angiotensin and its
 A:Reference number: A90917; M0ID:74127845
 A:Accession: A90917
 A:Molecule type: protein
 A:Residues: 1-10 <NAK>
 C:Keywords: blood pressure control; hormone; vasoconstrictor
 F:1-10/Product: angiotensin I #status experimental <ANI>
 F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.9%; Score 46; DB 2; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.0066;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 1 DRVYVHPF 8

RESULT 10
 A030345
 angiotensin precursor - bovine (fragment)
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 30-Oct-1992 #sequence_revision 30-Oct-1992 #text_change 20-Mar-1998
 C:Accession: A90345; A01250
 R:Elliot, D.F.; Peart, W.S.
 Biochem. J. 65: 246-254, 1957
 A>Title: The amino acid sequence in a hypertensin.
 A:Reference number: A90345
 A:Accession: A90345
 A:Molecule type: protein
 A:Residues: 1-10 <ELD>
 C:Keywords: blood pressure control; hormone; vasoconstrictor
 F:1-10/Product: angiotensin I #status experimental <ANI>
 F:1-8/Product: angiotensin II #status experimental <AN2>

Query Match 97.9%; Score 46; DB 2; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.0066;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 1 DRVYVHPF 8

RESULT 11
 S07207
 Crinia-angiotensin, skin - frog (Crinia georgiana)
 C:Species: Crinia georgiana
 C>Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 18-Aug-2000
 C:Accession: S07207
 R:Erspamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.
 Experientia 35: 1132-1133, 1979
 A>Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-1
 A:Reference number: S07207; M0ID:80024575
 A:Accession: S07207
 A:Molecule type: protein
 A:Residues: 1-11 <ERS>
 C:Superfamily: unassigned animal peptides

Query Match 95.7%; Score 45; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 0.011;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 4 DRVYVHPF 11

RESULT 12
 S72233
 transcription factor tbx6 - mouse
 C:Species: Mus musculus (house mouse)
 C>Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 05-Nov-1999
 C:Accession: S72233; S72232
 R:Agulnik, S.I.; Chapman, D.L.; Hancock, S.; Silver, L.M.
 submitted to the EMBL Data Library, May 1996
 A:Reference number: S72233
 A:Accession: S72233
 A:Molecule type: mRNA
 A:Residues: 1-540 <AGU>
 A:Cross-references: EMBL:U57331; NID:g1620601; PIDN:AAC53110.1; PID:g1620602
 R:Agulnik, S.I.; Garvey, N.; Hancock, S.; Ruvinsky, I.; Chapman, D.L.; Agulnik, I.; B
 Genetics 144: 249-254, 1996
 A>Title: Evolution of mouse T-box genes by tandem duplication and cluster dispersion.
 A:Reference number: S72230; M0ID:97032942
 A:Accession: S72232
 A>Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 100-280 <AGW>
 A:Cross-references: EMBL:U57331
 C:Genetics:
 A:Gene: tbx6
 C:Superfamily: T-box homology
 C:Keywords: DNA binding
 F:100-282/Domain: T-box homology <TBX>

Query Match 87.2%; Score 41; DB 2; Length 540;
 Best Local Similarity 100.0%; Pred. No. 4.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 7
 DB 170 DRVYIHPF 176

RESULT 13
 G81220
 hypothetical protein NMB0260 [imported] - Neisseria meningitidis (strain MC58 serogro
 C:Species: Neisseria meningitidis
 C>Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
 C:Accession: G81220
 R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
 Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
 Science 287: 1809-1815, 2000
 A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
 A>Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
 A:Reference number: A81000; M0ID:20175755
 A:Accession: G81220
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-128 <TER>
 A:Cross-references: GB:AE002382; GB:AE002098; NID:g7225470; PIDN:AAF40714.1; PID:g722
 C:Genetics:
 A:Experimental source: serogroup B, strain MC58
 A:Gene: NMB0260
 C:Superfamily: Neisseria meningitidis hypothetical protein NMB0260

Query Match 85.1%; Score 40; DB 2; Length 128;
 Best Local Similarity 62.5%; Pred. No. 1.5;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 DB 23 DRVYVHPF 30

RESULT 14

hypothetical protein XF0493 [imported] - Xylella fastidiosa (strain 9a5c)

C:Species: Xylella fastidiosa

C:Date: 18-Aug-2000 #sequence-revision 20-Aug-2000 #text-change 20-Aug-2000

C:Accession: F82800

R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: F82800

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-137 <SIM>

A:Cross-references: GB:AE003898; GB:AE003849; NID:g9105329; PIDN:AAE83303.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H

as-Melo, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigt

Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tsunako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF0493

Query Match

Best Local Similarity

Matches 5; Conservative

85.18; Score 40; DB 2; Length 132;

62.58; Pred. No. 1.6;

3; Mismatches

0; Indels

0; Gaps

0;

1 DRVYIHP 8

11111111

91 DRIVHHP 98

DB

RESULT 15

TBBO

thrombin (EC 3.4.21.5) precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 24-Apr-1984 #sequence-revision 14-Jul-1994 #text-change 18-Jun-1999

C:Accession: S02537; A00915; A37552; I46045; S67518

R:Irwin, D.M.; Robertson, K.A.; Macgillivray, R.T.A.

J. Mol. Biol. 200, 31-45, 1988

A:Title: Structure and evolution of the bovine prothrombin gene.

A:Reference number: S02537; MUID:88245190

A:Accession: S02537

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-625 <IRW>

R:Macgillivray, R.T.A.; Davie, E.W.

Biochemistry 23, 1626-1634, 1984

A:Title: Characterization of bovine prothrombin mRNA and its translation product.

A:Reference number: A00915; MUID:84203525

A:Accession: A00915

A:Molecule type: mRNA

A:Residues: 1-230, 'H', 232-625 <MAC>

A:Note: 600-Asn was also found

R:Magnusson, S.; Sottrop-Jensen, L.; Petersen, T.E.; Claeys, H.

In Boerhave Symposium on Prothrombin and Related Coagulation Factors, Hemker, H.C., and

A:Reference number: A37552

A:Accession: A37552

A:Molecule type: protein

A:Residues: 44-287, 'N', 289-352, 'E', 354, 'Q', 356-548, 'ND', 551-599, 'N', 601-625 <MAC>

A:Note: the evidence for 231-Ser is strong

A:Note: disulfide bonds and carbohydrate binding sites were determined

R:Park, C.H.; Tulinsky, A.

Biochemistry 25, 3977-3982, 1986

A:Title: Three-dimensional structure of the kringle sequence: structure of prothrombi

A:Reference number: A37553; MUID:86296631

A:Contents: annotation; residues 44-317, X-ray crystallography, 2.8 angstroms

R:Irwin, D.M.; Aherne, K.G.; Pearson, G.D.; Macgillivray, R.T.A.

Biochemistry 24, 6854-6861, 1985

A:Title: Characterization of the bovine prothrombin gene.

A:Reference number: A37554; MUID:86077733

A:Contents: annotation; gene structure

R:Macgillivray, R.T.; Degen, S.J.; Chandra, T.; Moo, S.L.; Davie, E.W.

Proc. Natl. Acad. Sci. U.S.A. 77, 5153-5157, 1980

A:Title: Cloning and analysis of a cDNA coding for bovine prothrombin.

A:Reference number: I46045; MUID:81054926

A:Accession: I46045

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 466-599, 'N', 601-625 <MA2>

A:Cross-references: EMBL:V00135; NID:g7772; PIDN:CAA23451.1; PID:g808945

R:Pejler, G.; Karlstroem, A.R.; Beig, L.

Eur. J. Biochem. 227, 102-107, 1995

A:Title: Identification of the proteolytic thrombin fragments formed after cleavage w

A:Reference number: S67518; MUID:95154277

A:Accession: S67518

A>Status: preliminary

A:Molecule type: protein

A:Residues: 318-325;333-338, 'X', 340;367-374;481-484, 'X', 486-488;515-522 <PBT>

A:Comment: Thrombin, which cleaves bonds after Arg and Lys, converts fibrinogen to fi

C:Comment: Prothrombin is activated on the surface of a phospholipid membrane that bl

itivation peptide and cleaves the remaining part into light and heavy chains. The acti

C:Comment: Thrombin can cleave the amino-terminal activation peptide 1 from prothromb

C:Comment: The gamma-carboxylglutamy1 residues bind calcium ions, result from the carb

ent interaction with the negatively charged phospholipid membrane surface.

C:Comment: The prothrombin precursor is synthesized in the liver.

C:Superfamily: thrombin; Gla domain homology; kringle homology; trypsin homology

C:Keywords: blood coagulation; calcium binding; carboxylglutamic acid; duplication; gl

F:1-24/Domain: signal sequence #status predicted <PRO>

F:25-43/Domain: propeptide #status predicted <PRO>

F:44-625/Product: prothrombin #status experimental <MP1>

F:44-199/Domain: activation peptide 1 #status experimental <FR1>

F:109-187/Domain: kringle homology <KR1>

F:200-317/Domain: activation peptide 2 #status experimental <FR2>

F:214-292/Domain: kringle homology <KR2>

F:318-366/Product: thrombin light chain #status experimental <LCH>

F:367-625/Product: thrombin heavy chain #status experimental <HCH>

F:367-616/Domain: trypsin homology <TRY>

F:50-51;58;60;63;64;69;70;73;76/Modified site: gamma-carboxylglutamic acid (Glu) #stat

F:61-66;91-104;109-187;130-170;158-182;214-292;235-275;263-287;339-485;394-410;539-55

F:120;144;419/Binding site: carboxylate (Asn) (covalent) #status experimental

F:409;465;571/Active site: His, Asp, Ser #status experimental

Query Match

Best Local Similarity

Matches 5; Conservative

78.7%; Score 37; DB 1; Length 625;

71.4%; Pred. No. 32;

2; Mismatches

0; Indels

0; Gaps

0;

1 DRVYIHP 7

11111111

448 DRIVYHP 454

DB

Search completed: May 24, 2002, 09:47:04

Job time: 44 sec

Fri May 24 13:12:21 2002

us-09-784-005-1.rpt

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 24, 2002, 09:47:05 ; Search time 10.37 seconds
(without alignments)
29.870 Million cell updates/sec

Title: US-09-784-005-1

Perfect score: 47
Sequence: 1 DRVYIHPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	100.0	8	1	ANG2_BOVJA
2	47	100.0	14	1	ANGT_HORSE
3	47	100.0	476	1	ANGT_SHEEP
4	47	100.0	477	1	ANGT_MOUSE
5	47	100.0	477	1	ANGT_RAT
6	47	100.0	485	1	ANGT_HUMAN
7	46	97.9	10	1	ANG1_BOVJA
8	46	97.9	10	1	ANGT_BOVIN
9	46	97.9	10	1	ANGT_CHICK
10	45	95.7	11	1	ANGT_CRIGE
11	41	87.2	436	1	TXB6_HUMAN
12	41	87.2	540	1	TXB6_MOUSE
13	37	78.7	625	1	THRB_BOVIN
14	35	74.5	305	1	END4_ARCFU
15	35	74.5	501	1	TX18_HUMAN
16	35	74.5	602	1	TX15_MOUSE
17	35	74.5	613	1	TX18_MOUSE
18	35	74.5	1355	1	VG46_HSV1
19	34	72.3	360	1	STPD_YEAST
20	34	72.3	481	1	Y335_SYNY3
21	34	72.3	525	1	GVAA_PSEAE
22	34	72.3	1224	1	RPOD_PITNH
23	34	72.3	3110	1	LM42_HUMAN
24	33	70.2	178	1	BDH_BOVIN
25	33	70.2	332	1	GALE_STRNR
26	33	70.2	333	1	GALE_STRMU
27	33	70.2	422	1	THD1_BACSU
28	33	70.2	465	1	Y093_RHME
29	33	70.2	510	1	PMGI_PSESM
30	33	70.2	528	1	GD_DROME
31	33	70.2	617	1	THRB_RAT
32	33	70.2	622	1	THRB_HUMAN
33	33	70.2	681	1	THR1_MOUSE

34	33	70.2	682	1	THR1_HUMAN	Q1650	homo sapien
35	33	70.2	695	1	CASP_MESAV	P1516	mesocricetu
36	33	70.2	743	1	YN02_CAEEL	Q03606	caenorhabdi
37	33	70.2	1071	1	CARB_BACSU	P25994	bacillus su
38	33	70.2	1149	1	HDA6_MOUSE	O922V5	mus musculu
39	33	70.2	1215	1	HDA6_HUMAN	O94077	homo sapien
40	32	68.1	78	1	FER_TRETH	P03942	thermus agu
41	32	68.1	177	1	Y404_TREPA	O83419	treponema p
42	32	68.1	288	1	GIL2_ENTHI	Q03077	entamoeba h
43	32	68.1	294	1	UP08_ECOLI	P39173	escherichia
44	32	68.1	304	1	Y191_METTH	O26293	methanobact
45	32	68.1	327	1	COO3_CANAL	O93995	c hexapreny

ALIGNMENTS

RESULT 1
ID ANG2_BOVJA STANDARD; PRT; 8 AA.
AC Q10582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Angiotensin-like peptide II (Fragment).
OS Bothrops jararaca (Jararaca).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidae;
OC Viperidae; Crotalinae; Bothrops.
OX NCBI_TaxID=8724;
RN [1]
RP SEQUENCE.
RC TISSUE=Plasma;
RX MEDLINE=96208932; PubMed=8829801;
RA Borgegessi R.A.M.B., Dalle Lucca J., Carmona E., Picarelli Z.P.;
RT "Isolation and identification of angiotensin-like peptides from the
RT plasma of the snake Bothrops jararaca".
RL Comp. Biochem. Physiol. 113B:467-473(1996).
CC -I- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
DR InterPro: IPR000215; Serpin.
DR PROSITE: PS00284; SERPIN; PARTIAL.
KW Vasoconstrictor; Plasma; Serpin.
FT NON_TER
SQ SEQUENCE 8 AA: 1046 MW: DDD761E04B42D40A CRC64;

Query Match 100.0%; Score 47; DB 1; Length 8;
Best Local Similarity 100.0%; Pred. No. 1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRVYIHPF 8
DQ 1 DRVYIHPF 8

RESULT 2
ID ANGT_HORSE STANDARD; PRT; 14 AA.
AC P01016;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Angiotensinogen (Contains: Angiotensin I; Angiotensin II) (Fragment).
GN SERPINA8 OR AGT.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;
RN [1]
RP SEQUENCE.
RA Skeggs L.T. Jr., Kahn J.R., Lentz K., Shumway N.P.;
RT "The preparation, purification, and amino acid sequence of a
polypeptide renin substrate.";

RL J. Exp. Med. 106:439-453(1957).

CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.

CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

DR PIR: A01250; A01250.

DR InterPro: IPR000215; Serpin.

DR PROSITE: PS00284; SERPIN; PARTIAL.

KM Vasoconstrictor; Plasma; Serpin.

FT PEPTIDE 1 10 ANGIOTENSIN I.

FT NON_TER 1 8 ANGIOTENSIN II.

FT SEQUENCE 14 AA; 1759 MW; 2E9921F8EEFBDD7 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 0.0035;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
 Db 1 DRYIHPF 8

RESULT 3
 ANGT_SHEEP
 ID ANGT_SHEEP STANDARD; PRT; 476 AA.
 AC P20757;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
 GN SERPIN8 OR AGT
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 OX NCBI_TaxID=9940;
 RN [1]
 RP TISSUE=Liver;
 RC MEDLINE=95072318; PubMed=7765514;
 RA Nagase M., Suzuki F., Fukamizu A., Takeda N., Takeuchi K.,
 RA Murakami K., Nakamura Y.;
 RT "Sequencing and expression of sheep angiotensinogen cDNA."
 RL Biosci. Biotechnol. Biochem. 58:1884-1885(1994).
 RM [2]
 RP SEQUENCE OF 25-39.
 RX MEDLINE=86136099; PubMed=3081342;
 RA Fernley R.T., John M., Niall H.D., Coghlan J.P.;
 RT "Purification and characterization of ovine angiotensinogen."
 RL Eur. J. Biochem. 154:597-601(1986).

CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.

CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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DR EMBL: D17520; BAA04470.1; -
 DR PIR: A25406; A25406.
 DR InterPro: IPR000227; Angiotensngn.
 DR InterPro: IPR000215; Serpin.
 DR PIR: P00079; serpin.1.
 DR PRINTS: PR00654; ANGIOTENSNGN.
 DR SMART: SM00093; SERPIN.1.
 DR PROSITE: PS00284; SERPIN; 1.
 KM Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 476 ANGIOTENSINOGEN.
 FT PEPTIDE 25 34 ANGIOTENSIN I.
 FT PEPTIDE 25 32 ANGIOTENSIN II.
 FT CARBOHYD 295 295 N-LINKED (GLCNAC...) (POTENTIAL).
 FT SEQUENCE 476 AA; 51304 MW; C8A517CD9FA029F7 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
 Db 25 DRYIHPF 32

RESULT 4
 ANGT_MOUSE
 ID ANGT_MOUSE STANDARD; PRT; 477 AA.
 AC P11859;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
 GN SERPIN8 OR AGT.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88284703; PubMed=3397061;
 RA Clouston W.M., Evans B.A., Haralambidis J., Richards R.I.;
 RT "Molecular cloning of the mouse angiotensinogen gene."
 RL Genomics 2:240-248(1988).

CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.

CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.

CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.

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 CC or send an email to license@isb-sib.ch).

CC EMBL: AF045887; AAC01765.1; -
 DR EMBL: AF045886; AAC01765.1; JOINED.
 DR EMBL: AF045885; AAC01765.1; JOINED.
 DR EMBL: AF045884; AAC01765.1; JOINED.
 DR PIR: A29978; A29978.
 DR MGD: MGI:87963; Agt.
 DR InterPro: IPR000227; Angiotensngn.
 DR InterPro: IPR000215; Serpin.
 DR PIR: P00079; serpin.1.
 DR PRINTS: PR00654; ANGIOTENSNGN.
 DR SMART: SM00093; SERPIN.1.

DR PROSITE: PS00284; SERPIN; FALSE_NEG.
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 477
 FT PEPTIDE 25 34
 FT CARBOHYD 38 38
 FT CARBOHYD 319 319
 FT CARBOHYD 401 401
 SO SEQUENCE 477 AA; 51990 MW; A877F4029F338607 CRC64;

Query Match 100.0%; Score 47; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
 Db 25 DRYIHPF 32

RESULT 5
 ANGT_RAT STANDARD; PRT; 477 AA.
 ID ANGT_RAT
 AC P01015;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
 GN SERPINB8 OR AGT.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WISTR; MEDLINE=83169849; PubMed=6572971;
 RA Okubo H., Kageyama R., Ujihara M., Hirose T., Inayama S.,
 RA Nakanishi S.;
 RT "Cloning and sequence analysis of cDNA for rat angiotensinogen.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:2196-2200(1983).
 RN [2]
 RP SEQUENCE OF 25-34.
 RA MEDLINE=73060322; PubMed=4344907;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. II. Structure of rat
 angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 20:1579-1581(1972)
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC
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 CC
 DR EMBL: L00094; AAA98779.1;
 DR EMBL: L00091; AAA98778.1; JOINED.
 DR EMBL: L00092; AAA98779.1; JOINED.
 DR EMBL: L00093; AAA98779.1; JOINED.
 DR PIR: A01251; ANRT.
 DR InterPro: IPR000227; Angiotensin.
 DR InterPro: IPR000215; Serpin.

DR Pfam: PF00079; serpin; 1.
 DR PRINTS: PR00654; ANGIOTENSNGN.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; FALSE_NEG.
 KW Vasoconstrictor; Glycoprotein; Plasma; Serpin; Signal.
 FT SIGNAL 1 24
 FT CHAIN 25 477
 FT PEPTIDE 25 34
 FT CARBOHYD 38 38
 FT CARBOHYD 319 319
 FT CARBOHYD 401 401
 SO SEQUENCE 477 AA; 51981 MW; 689051A578BD693D CRC64;

Query Match 100.0%; Score 47; DB 1; Length 477;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8
 Db 25 DRYIHPF 32

RESULT 6
 ANGT_HUMAN STANDARD; PRT; 485 AA.
 ID ANGT_HUMAN
 AC P01019; Q16358; Q16359;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen precursor [Contains: Angiotensin I; Angiotensin II].
 GN SERPINB8 OR AGT.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=89170129; PubMed=2924688;
 RA Gaillard I., Clausen E., Corvol P.;
 RT "Structure of human angiotensinogen gene.";
 RL DNA 8:87-99(1989).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=85000455; PubMed=6089875;
 RA Kageyama R., Okubo H., Nakanishi S.;
 RT "Primary structure of human preangiotensinogen deduced from the
 RT cloned cDNA sequence.";
 RL Biochemistry 23:3603-3609(1984).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=90237063; PubMed=1692023;
 RA Fukunaga A., Takahashi S., Seo M.S., Tada M., Tanimoto K., Uehara S.,
 RA Murakami K.;
 RT "Structure and expression of the human angiotensinogen gene.
 RT Identification of a unique and highly active promoter.";
 RL J. Biol. Chem. 265:7576-7582(1990).
 RN [4]
 RP SEQUENCE OF 1-338 FROM N.A.
 RA MEDLINE=87244745; PubMed=2885106;
 RA Kunapuli S.P., Kumar A.;
 RT "Molecular cloning of human angiotensinogen cDNA and evidence for the
 RT presence of its mRNA in rat heart.";
 RL Circ. Res. 60:786-790(1987).
 RN [5]
 RP SEQUENCE OF 34-45, AND SUBUNITS.
 RC TISSUE-Serum;
 RA MEDLINE=95293954; PubMed=7539791;
 RA Oxyg C., Haaning J., Kristensen L., Wagner J.M., Rubin I.,
 RA Stigbrand T., Gleish G.J., Sottrup-Jensen L.;
 RT "Identification of angiotensinogen and complement C3dg as novel
 RT proteins binding the proform of eosinophil major basic protein in
 human pregnancy serum and plasma.";

RN J. Biol. Chem. 270:13645-13651(1995).
 RN [6]
 RP SEQUENCE OF 34-43.
 RX MEDLINE=69014170; PubMed=4300938;
 RA Arakawa K., Minohara A., Yamada J., Nakamura M.;
 RT "Enzymatic degradation and electrophoresis of human angiotensin I.";
 RN Biochim. Biophys. Acta 168:106-112(1968).
 RN [7]
 RP STRUCTURE BY NMR OF ANGIOTENSIN II.
 RX MEDLINE=98151281; PubMed=9492317.
 RA Carpenter K.A., Wilkes B.C., Schiller P.W.;
 RT "The octapeptide angiotensin II adopts a well-defined structure in a
 phospholipid environment";
 RN Eur. J. Biochem. 251:448-453(1998).
 RN [8]
 RP VARIANTS MET-207; THR-268 AND CYS-281.
 RX MEDLINE=93008239; PubMed=1394429.
 RA Jeunemaitre X., Soubrier F., Kotelevtsev V.V., Lifton R.P.,
 RA Williams C.S., Charru A., Hunt S.C., Hopkins P.N., Williams R.R.,
 RT "Molecular basis of human hypertension: role of angiotensinogen.";
 RN Cell 71:169-180(1992).
 RN [9]
 RP VARIANT THR-268.
 RX MEDLINE=93291876; PubMed=8513325;
 RA Ward K., Hata A., Jeunemaitre X., Helin C., Nelson L., Namikawa C.,
 RA Farrington P.F., Ogasawara M., Suzumori K., Tomoda S., Berrebi S.,
 RA Sasaki M., Corvol P., Lifton R.P., Lalouel J.-M.;
 RT "A molecular variant of angiotensinogen associated with
 preclampsia";
 RN Nat. Genet. 4:59-61(1993).
 RN [10]
 RP VARIANTS ILE-242; ARG-244 AND CYS-281.
 RX MEDLINE=95331754; PubMed=7607642;
 RA Hixson J.E., Powers P.K.;
 RT "Detection and characterization of new mutations in the human
 angiotensinogen gene (AGT).";
 RN Hum. Genet. 96:110-112(1995).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN, ACE (ANGIOTENSIN
 CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 BALANCE OF BODY FLUIDS.
 CC -1- SUBUNIT: During pregnancy, exists as a disulfide-linked 2:2
 heterotrimer with the proform of PRG2 and as a complex (probably
 a 2:2:2 heterotrimer) with pro-PRG2 and C3dg.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- DISEASE: AGT SEEMS TO BE ASSOCIATED WITH A PREDISPOSITION TO
 ESSENTIAL HYPERTENSION AS WELL AS PREGNANCY-INDUCED HYPERTENSION
 (PIH) (PRECLAMPSIA).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-10 IS THE INITIATOR.
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 CC -----
 DR EMBL: K02215; AA51731.1; -
 DR EMBL: M24689; AA51679.1; -
 DR EMBL: M24686; AA51679.1; JOINED.
 DR EMBL: M24687; AA51679.1; JOINED.
 DR EMBL: M24688; AA51679.1; JOINED.
 DR EMBL: X15324; CA33385.1; JOINED.
 DR EMBL: X15325; CA33385.1; JOINED.
 DR EMBL: X15326; CA33385.1; JOINED.
 DR EMBL: X15327; CA33385.1; JOINED.
 DR EMBL: M69110; AA52282.1; -
 DR EMBL: S78529; AAD14287.1; -

DR EMBL: S78530; AAD14288.1; -
 DR PIR: A01249; ANHU.
 DR PIR: A31362; A31362.
 DR PIR: A35203; A35203.
 DR SWISS-2DPAGE: P01019; HUMAN.
 DR MIM: 106150; -
 DR InterPro: IPR000227; Angiotensin.
 DR InterPro: IPR000215; Serpin.
 DR Pfam: PF00079; serpin_1.
 DR PRINTS: PR00654; ANGIOTENSNGN.
 DR SMART: SM00093; SERPIN; 1.
 DR PROSITE: PS00284; SERPIN; 1.
 KW Vasocostrictor; Glycoprotein; Plasma; Serpin; Signal;
 KW Disease mutation; Polymorphism.
 FT SIGNAL 1 33
 FT CHAIN 34 485
 FT PEPTIDE 34 43
 FT PEPTIDE 34 41
 FT CARBOHYD 47 47
 FT CARBOHYD 170 170
 FT CARBOHYD 304 304
 FT CARBOHYD 328 328
 FT CARBOHYD 207 207
 FT VARIANT 242 242
 FT VARIANT 244 244
 FT VARIANT 268 268
 FT VARIANT 281 281
 FT CONFLICT 333 333
 FT SEQUENCE 485 AA; 53154 MW; 5026C2DFB2DD336E CRC64;
 SQ
 Query Match 100.0%; Score 47; DB 1; Length 485;
 Best local Similarity 100.0%; Pred. No. 0.12;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRYIIHPF 8
 DB 34 DRYIIHPF 41
 RESULT 7
 ID ANGL_BOTJA STANDARD; PRT; 10 AA.
 AC Q10581;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Angiotensin-like peptide I (Fragment).
 OS Bothrops jararaca (Jararaca).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea;
 OC Viperidae; Crotalinae; Bothrops.
 DE NCBI_TaxID=8724;
 RP [1]
 RP SEQUENCE.
 RC TISSUE=Plasma;
 RX MEDLINE=96208932; PubMed=8829801;
 RA Borgheresi R.A.M.B., Dalle Luccha J., Garmona E., Picarelli Z.P.;
 RT "Isolation and identification of angiotensin-like peptides from the
 RT plasma of the snake Bothrops jararaca";
 RL Comp. Biochem. Physiol. 113B:467-473(1996).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 CC InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN; PARTIAL.
 KW Vasocostrictor; Plasma; Serpin.
 FT NON_TER 10
 FT SEQUENCE 10 AA; 1308 MW; CEF50DD761F2DB42 CRC64;

Query Match 97.9%; Score 46; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.0038;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVHPF 8
 ||||:||||
 DB 1 DRYVHPF 8

RESULT 8
 ID ANGT_BOVIN STANDARD; PRT; 10 AA.
 AC P01017;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen [contains: Angiotensin I; Angiotensin II] (Fragment).
 GN SERPINB8 OR AGT.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RA Elliott D.F., Peart W.S.;
 RT "The amino acid sequence in a hypertensin.";
 RL Biochem. J. 65:246-254(1957).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A01250; A01250.
 DR PIR: A90345; A90345.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN, PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 DR VASOCONSTRICTOR; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT NON_TER 10 8 ANGIOTENSIN II.
 FT SEQUENCE 10 AA; 1282 MW; CEEFBD761FZDB42 CRC64;

Query Match 97.9%; Score 46; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.0038;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVHPF 8
 ||||:||||
 DB 1 DRYVHPF 8

RESULT 9
 ID ANGT_CHICK STANDARD; PRT; 10 AA.
 AC P01018;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Angiotensinogen [contains: Angiotensin I; Angiotensin II] (Fragment).
 GN SERPINB8 OR AGT.
 OS Gallus gallus (Chicken), and
 OS Coturnix coturnix japonica (Japanese quail).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031, 93934;
 RN [1]

RP SEQUENCE.
 RC SPECIES=Chicken;
 RX MEDLINE=74127845; PubMed=4361802;
 RA Nakayama T., Nakajima T., Sokabe H.;
 RT "Comparative studies on angiotensins. 3. Structure of fowl
 RT angiotensin and its identification by DNS-method.";
 RL Chem. Pharm. Bull. 21:2085-2087(1973).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.c.japonica;
 RX MEDLINE=90284684; PubMed=2191893;
 RA Takel Y., Hasegawa Y.;
 RT "Vasopressor and depressor effects of native angiotensins and
 RT inhibition of these effects in the Japanese quail.";
 RL Gen. Comp. Endocrinol. 79:12-22(1990).
 CC -1- FUNCTION: IN RESPONSE TO LOWERED BLOOD PRESSURE, THE ENZYME RENIN
 CC CLEAVES ANGIOTENSIN I, FROM ANGIOTENSINOGEN. ACE (ANGIOTENSIN
 CC CONVERTING ENZYME) THEN REMOVES A DIPEPTIDE TO YIELD THE
 CC PHYSIOLOGICALLY ACTIVE PEPTIDE ANGIOTENSIN II, THE MOST POTENT
 CC PRESSOR SUBSTANCE KNOWN, WHICH HELPS REGULATE VOLUME AND MINERAL
 CC BALANCE OF BODY FLUIDS.
 CC -1- TISSUE SPECIFICITY: MADE IN THE LIVER & SECRETED IN THE PLASMA.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR PIR: A01250; A01250.
 DR PIR: A90917; A90917.
 DR PIR: A60624; A60624.
 DR InterPro: IPR000215; Serpin.
 DR PROSITE: PS00284; SERPIN, PARTIAL.
 KW Vasoconstrictor; Plasma; Serpin.
 FT PEPTIDE 1 10 ANGIOTENSIN I.
 FT NON_TER 10 8 ANGIOTENSIN II.
 FT SEQUENCE 10 AA; 1232 MW; CEEFBD761FZDB42 CRC64;

Query Match 97.9%; Score 46; DB 1; Length 10;
 Best Local Similarity 87.5%; Pred. No. 0.0038;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVHPF 8
 ||||:||||
 DB 1 DRYVHPF 8

RESULT 10
 ID ANGT_CRIGE STANDARD; PRT; 11 AA.
 AC P09037;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Crinia angiotensin II.
 GN Crinia georgiana (Quacking frog).
 OS Crinia georgiana (Quacking frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Myobatrachidae;
 OC Crinia.
 OX NCBI_TaxID=8374;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=80024575; PubMed=488254;
 RA Espamer V., Melchiorri P., Nakajima T., Yasuhara T., Endean R.;
 RT "Amino acid composition and sequence of crinia-angiotensin, an
 RT angiotensin II-like endecapeptide from the skin of the Australian
 RT frog Crinia georgiana.";
 RL Experientia 35:1132-1133(1979).
 DR PIR: S07207; S07207.
 KW Vasoconstrictor.
 FT SEQUENCE 11 AA; 1271 MW; 8A0921F7DB50440A CRC64;

Query Match 95.7%; Score 45; DB 1; Length 11;
 Best Local Similarity 75.0%; Pred. No. 0.0065;

Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DRVYIHPF 8
 ||:||||
 Db 4 DRVYHPF 11

RESULT 11

TBX6_HUMAN

ID TBX6_HUMAN STANDARD; PRT; 436 AA.

AC O95947;

DT 15-JUL-1999 (Rel. 38, Created)

DT 15-JUL-1999 (Rel. 38, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE T-box transcription factor TBX6 (T-box protein 6).

GN TBX6.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-99134303; PubMed-993572;

RT Papapetrou C., Putt W., Fox M., Edwards Y.H.;

RL "The human TBX6 gene: cloning and assignment to chromosome 16p11.2,"

Genomics 55:238-241(1999).

RN [2]

RP SEQUENCE OF 135-272 FROM N.A.

RC TISSUE=Myeloid;

RX MEDLINE-99107806; PubMed-9888994;

RA Yl C.H., Terrett J.A., Li Q.-Y., Ellington K., Packham E.A.,

RT "Amstrong-Buisseret L., McClure P., Slingsby T., Brook J.D.,"

RT "Identification, mapping and phylogenetic analysis of four new human

RT members of the T-box gene family: BOMES, TBX6, TBX18, and TBX19,"

Genomics 55:10-20(1999).

RL [1]

RP FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN

DEVELOPMENTAL PROCESSES. COULD BE REQUIRED FOR SPECIFICATION OF

PARAXIAL MESODERM STRUCTURES DURING GASTRULATION (BY SIMILARITY).

CC -1- SUBUNIT: FORMS A DIMERIC COMPLEX WITH DNA (IN VITRO).

CC -1- TISSUE SPECIFICITY: EXPRESSED IN FETAL TAIL BUD, POSTERIOR SPINAL

CC TISSUE, INTERVENTRICAL DISC AND TESTIS. ALSO EXPRESSED IN ADULT

CC TESTIS, KIDNEY, LUNG, MUSCLE AND THYMUS.

CC -1- DEVELOPMENTAL STAGE: EXPRESSED DURING GASTRULATION AND DURING A

CC SECOND PHASE IN SOME ADULT TISSUES.

CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: AJ007989; CA007812.1; -

CC EMBL: AJ010279; CAB37938.1; -

CC HSSP: P24781; 1XBR.

CC MIM: 602427; -

CC InterPro: IPR001699; T-box.

CC Pfam: PF00907; T-box.

CC PRINTS: PR00937; TBOX.

CC SMART: SM00425; TBOX.1.

CC PROSITE: PS01283; TBOX.1; 1.

CC PROSITE: PS01264; TBOX.2; 1.

CC PROSITE: PS50252; TBOX.3; 1.

CC Transcription regulation; DNA-binding; Nuclear protein;

CC Developmental protein.

CC DNA_BIND 100 273 T-BOX.

CC FT CONFLICT 207 207 H -> HV (IN REF. 2).

CC SEQUENCE 436 AA; 47017 MW; 43817BBD1B966E9 CAC64;

Query Match 87.2%; Score 41; DB 1; Length 436;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

TBX6_MOUSE

ID TBX6_MOUSE STANDARD; PRT; 540 AA.

AC P70327;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE T-box transcription factor TBX6 (T-box protein 6).

GN TBX6.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE-97032942; PubMed-8878690;

RT Aguilnik S.I., Garvey N., Hancock S., Ruvinsky I., Chapman D.L.,

RT "Evolution of mouse T-box genes by tandem duplication and cluster

RT dispersion,"

Genetics 144:249-254(1996).

RN [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Gastrula;

RX MEDLINE-97115702; PubMed-8954725;

RA Chapman D.L., Aguilnik I., Hancock S., Silver L.M., Papaioannou V.E.;

RT "Tbx6, a mouse T-box gene implicated in paraxial mesoderm formation at

RT gastrulation,"

Dev. Biol. 180:534-542(1996).

RN [3]

RP FUNCTION.

RA MEDLINE-98140705; PubMed-9490412;

RT Chapman D.L., Papaioannou V.E.;

RT "Three neutral tubes in mouse embryos with mutations in the T-box gene

RT Tbx6,"

Nature 391:695-697(1998).

CC -1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN

CC DEVELOPMENTAL PROCESSES. REQUIRED FOR SPECIFICATION OF PARAXIAL

CC MESODERM STRUCTURES DURING GASTRULATION. IN ITS ABSENCE CELLS

CC DESTINED TO FORM POSTERIOR SOMITES DIFFERENTIATE ALONG A NEURONAL

CC PATHWAY.

CC -1- SUBCELLULAR LOCATION: Nuclear (potential).

CC -1- DEVELOPMENTAL STAGE: TBX6 IS FIRST DETECTED IN THE GASTRULATION

CC STAGE IN THE PRIMITIVE STREAK AND NEWLY RECRUITED PARAXIAL

CC PARAXIAL MESODERM AND TO THE TAIL BUD, WHICH REPLACES THE STREAK

CC AS THE SOURCE OF MESODERM.

CC -1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

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CC -----

CC EMBL: U57331; AAC53110.1; -

CC HSSP: P24781; 1XBR.

CC MGD: MGI:102539; Tbx6.

CC InterPro: IPR001699; T-box.

CC Pfam: PF00907; T-box.1.

CC PRINTS: PR00937; TBOX.

DR SMART: SM00425; TB0X: 1.
 DR PROSITE; PS01283; TB0X_1: 1.
 DR PROSITE; PS01284; TB0X_2: 1.
 DR PROSITE; PS0252; TB0X_3: 1.
 DR Transcription regulation; DNA-binding; Nuclear protein;
 KM Developmental protein.
 FT DOMAIN 61 64 POLY-ALA.
 FT DOMAIN 79 82 POLY-PRO.
 FT DOMAIN 100 273 T-BOX.
 SQ SEQUENCE 540 AA; 58628 MW; BC834CE2745EBE61 CRC64;

Query Match 87.2%; Score 41; DB 1; Length 540.
 Best Local Similarity 100.0%; Pred. No. 1.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYHP 7
 |||||
 DB 170 DRVYHP 176

RESULT 13
 ID THRB_BOVIN STANDARD; PRT; 625 AA.
 AC P00735;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Prothrombin precursor (EC 3.4.21.5).
 OS F2.
 GN Bos taurus (Bovine).
 OC Chordata; Craniata; Euteleostomi;
 OC Eumetazoa; Metazoa; Cephalochordata; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=88245190; PubMed=3379642;
 Irwin D.M., Robertson K.A., McGallivray R.T.A.;
 "Structure and evolution of the bovine prothrombin gene.";
 J. Mol. Biol. 200;31:45(1988).
 [2]
 SEQUENCE FROM N.A.
 MEDLINE=84203525; PubMed=6326805;
 McGallivray R.T.A., Davie E.W.;
 "Characterization of bovine prothrombin mRNA and its translation
 product.";
 Biochemistry 23:1626-1634(1984).
 [3]
 SEQUENCE OF 44-625, DISULFIDE BONDS, AND CARBOHYDRATE-LINKAGE SITES.
 Magnusson S., Sottirup-Jensen L., Petersen T.E., Claess H.;
 (in) Hemker H.C., Veltkamp J.J. (eds.);
 Bernaabe symposium on prothrombin and related coagulation factors,
 pp.25-46, Leiden University Press, Leiden (1975).
 [4]
 X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 MEDLINE=86296631; PubMed=3741841;
 Park C.H., Tulinsky A.;
 "Three-dimensional structure of the kringle sequence: structure of
 prothrombin fragment 1.";
 Biochemistry 25:3977-3982(1986).
 [5]
 X-RAY CRYSTALLOGRAPHY (2.25 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 MEDLINE=91311686; PubMed=1856869;
 Seshadri T.-P., Tulinsky A., Skrzypczak-Jankun E., Park C.H.;
 "Structure of bovine prothrombin fragment 1 refined at 2.25-A
 resolution.";
 J. Mol. Biol. 220:481-494(1991).
 [6]
 X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF ACTIVATION PEPTIDE 1.
 MEDLINE=92190185; PubMed=1547238;
 Soriano-Garcia M., Padmanabhan K., de Vos A.M., Tulinsky A.;
 "The Ca2+ ion and membrane binding structure of the Gla domain of Ca-

RT prothrombin fragment 1.";
 RL Biochemistry 31:2554-2566(1992).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RX MEDLINE=92218459; PubMed=1560020;
 Martin P.D., Robertson W., Turk D., Huber R., Bode W., Edwards B.F.P.;
 "The structure of residues 7-16 of the A alpha chain of human
 fibrinogen bound to bovine thrombin at 2.3-A resolution.";
 J. Biol. Chem. 267:7911-7920(1992).
 RL [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RP MEDLINE=92389319; PubMed=1518046;
 Brandstetter H., Turk D., Hofliken H.W., Grosse D., Stuerzebecher J.,
 Martin P.D., Edwards B.F.P., Bode W.;
 "Refined 2.3 A X-ray crystal structure of bovine thrombin complexes
 formed with the benzamidine and arginine-based thrombin inhibitors
 NAPAP, 4-TAPAP and MQPA. A starting point for improving
 antithrombotics.";
 J. Mol. Biol. 226:1085-1089(1992).
 RN [9]
 RP X-RAY CRYSTALLOGRAPHY (3.1 ANGSTROMS) OF COMPLEX WITH ORNITHODORIN.
 RX MEDLINE=97102783; PubMed=8947023;
 van de locht A., Stubbs M.T., Bode W., Friedrich T., Bollschweiler C.,
 Hofliken W., Huber R.;
 "The ornithodorin-thrombin crystal structure, a key to the TAP
 enigma?";
 EMBO J. 15:6011-6017(1996).
 RN [10]
 RP X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF COMPLEX WITH TRIBIN.
 RX MEDLINE=98004486; PubMed=9342325;
 Fuentes-Prior P., Noeske-Jungblut C., Donner P., Schleuning W.D.,
 Huber R., Bode W.;
 "Structure of the thrombin complex with tribin, a lipocalin-like
 exosite-binding inhibitor derived from a tritonome bug.";
 Proc. Natl. Acad. Sci. U.S.A. 94:11845-11850(1997).
 RN [11]
 RP GENE STRUCTURE.
 MEDLINE=86077733; PubMed=3000440;
 Irwin D.M., Ahern K.G., Pearson G.D., McGallivray R.T.A.;
 "Characterization of the bovine prothrombin gene.";
 Biochemistry 24:6854-6861(1985).
 RL [12]
 RN FIBRINOGEN TO FIBRIN AND ACTIVATES FACTORS V, VII, VIII, XIII,
 CC AND, IN COMPLEX WITH THROMBOMODULIN, PROTEIN C.
 CC [13]
 CC SUBCELLULAR LOCATION: Extracellular.
 CC [14]
 CC TISSUE SPECIFICITY: SYNTHESIZED IN THE LIVER. FOUND IN PLASMA.
 CC [15]
 CC -1- PTM: THE GAMMA-CARBOXYGLUTAMYL RESIDUES, WHICH BIND CALCIUM IONS,
 CC RESULT FROM THE CARBOXYLATION OF GLUTAMYL RESIDUES BY A MICROSOMAL
 CC ENZYME, THE VITAMIN K-DEPENDENT CARBOXYLASE. THE MODIFIED RESIDUES
 CC ARE NECESSARY FOR THE CA-DEPENDENT INTERACTION WITH A NEGATIVELY
 CC CHARGED PHOSPHOLIPID SURFACE, WHICH IS ESSENTIAL FOR THE CONVERSION
 CC OF PROTHROMBIN TO THROMBIN.
 CC [16]
 CC MISCELLANEOUS: PROTHROMBIN IS ACTIVATED ON THE SURFACE OF A
 CC PHOSPHOLIPID MEMBRANE THAT BINDS THE AMINO END OF PROTHROMBIN &
 CC FACTORS VA & XA IN CA-DEPENDENT INTERACTIONS; FACTOR XA REMOVES
 CC THE ACTIVATION PEPTIDE & CLEAVES THE REMAINING PART INTO LIGHT &
 CC HEAVY CHAINS. THE ACTIVATION PROCESS STARTS SLOWLY BECAUSE FACTOR
 CC V ITSELF HAS TO BE ACTIVATED BY THE INITIAL, SMALL AMOUNTS OF
 CC THROMBIN.
 CC [17]
 CC MISCELLANEOUS: THROMBIN CAN ITSELF CLEAVE THE AMINO TERMINAL
 CC FRAGMENT (FRAGMENT 1) OF THE PROTHROMBIN, PRIOR TO ITS ACTIVATION
 CC BY FACTOR XA.
 CC [18]
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FT	MOD_RES	70	70	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	73	73	GAMMA-CARBOXYGLUTAMIC ACID.
FT	MOD_RES	76	76	GAMMA-CARBOXYGLUTAMIC ACID.
FT	CARBOHYD	120	120	N-LINKED (GLICNC. . .).
Query Match				
Best Local Similarity		78.7%;		
Matches		5; Conservative		
		Score 37; DB 1; Length 625;		
		Pred No 12;		
		Mismatches 0; Indels 0; Gaps 0;		
Oy	1 DRVYIHP	7		
	:::			
Db	448 DKYIHP	454		

Query Match

74.5%; Score 35; DB 1; Length 305.

Db 448 DKXTHP 454

RESULT 14
ID ENDA_ARCFU STANDARD; PRT; 305 AA.
AC 029362;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
GN ENDA OR AF0900.
OS Archaeoglobus fulgidus.
OC Archaeae; Euryarchaeota; Archaeoglobales; Archaeoglobaceae;
OX NCBI_TaxID=2234;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;
RX MEDLINE=98049343; PubMed=9389475;
RA Kleink H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,
RA Reichman K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,
RA Fleischmann D.L., Kerlavage A.R., Graham D.E., Kyriades N.C.,
RA Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Gill S.,
RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodok A., Zhou L.,
RA Cotton M.D., Spriggs T., Arltach P., Kalne B.P., Sykes S.M.,
RA Sadov F.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,
RA Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
RA Venter J.C.;
RT "The complete genome sequence of the hyperthermophilic, sulfate-
reducing archaeon Archaeoglobus fulgidus.";
RL Nature 390:364-370(1997).
CC -! FUNCTION: CLEAVES PRE-tRNA AT THE 5' AND 3' SPICE SITES TO
CC RELEASE THE INTRON. THE PRODUCTS ARE AN INTRON AND TWO TRNA HALF-
CC MOLECULES BEARING 2',3' CYCLIC PHOSPHATE AND 5'-OH TERMINI (BY
CC SIMILARITY).
CC -! CATALYTIC ACTIVITY: Endonucleolytic cleavage of pre-tRNA,
CC specifying 5'-hydroxyl and 2',3'-cyclic phosphate terminal, and
CC -! SIMILARITY: BELONGS TO THE TRNA-INTRON ENDONUCLEASE FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation-
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).

EMBL: AF001041; AAB90338.1; -
HSSP: Q58819; IA79.
TIGR: AF0900; -
InterPro: IPR002827; tRNA_int_endo.
Pfam: PF01974; tRNA_int_endo.N.1.
PFam: PF02778; tRNA_int_endo.N.1.
HydroLase: Nuclease; Endonuclease; tRNA processing; Complete proteome.
SEQUENCE 305 AA; 35959 MW; DC05A5ADEBD99E35 CRC64;

Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRVYIHP 7
|:|:|:|
Db 26 DKYLHP 32

Search completed: May 24, 2002, 09:50:38
Job time: 213 sec

RESULT 15

TX18_HUMAN

ID TX18_HUMAN

STANDARD;

PRT;

501 AA.

O95935; O9UJ16;

30-MAY-2000 (Rel. 39, Created)

16-OCT-2001 (Rel. 40, Last sequence update)

01-MAR-2002 (Rel. 41, Last annotation update)

T-box transcription factor TBX18 (T-box protein 18) (Fragment).

TBX18.

Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

NCBI_TaxID=9606;

[1]

SEQUENCE FROM N.A.

Bates K.;

Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

[2]

SEQUENCE OF 42-223 FROM N.A.

MEDLINE=99107806; PubMed=9888994;

Yi C.-H., Terrett J.A., Li O.-Y., Ellington K., Packham E.A.,

Amstrong-Balseret L., McClure P., Slingsby T., Brock J.D.;

"Identification, mapping and phylogenomic analysis of four new human

members of the T-box gene family: BOMES, TBX6, TBX18, and TBX19."

Genomics 55:10-20(1999).

-1- FUNCTION: PROBABLE TRANSCRIPTIONAL REGULATOR INVOLVED IN

DEVELOPMENTAL PROCESSES.

-1- SUBCELLULAR LOCATION: Nuclear (Potential).

-1- SIMILARITY: CONTAINS 1 T-BOX DOMAIN.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

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modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>or send an email to license@isb-sib.ch).

CC EMBL; AL035694; CAB45196.1; -

CC EMBL; AJ010278; CAB37937.1; -

CC HSSP; P24781; 1XBR.

CC MIM; 604613; -

CC InterPro: IPR001699; T-box.

CC Pfam: PF00907; T-box; 1.

CC PRINTS; PR00937; TBOX.

CC SMART; SM00425; TBOX; 1.

CC PROSITE; PS01283; TBOX_1; 1.

CC PROSITE; PS01264; TBOX_2; 1.

CC PROSITE; PS0252; TBOX_3; 1.

CC Transcription regulation; DNA-binding; Nuclear protein.

KW NON_TER 1

FT DNA_BIND 42 224 T-BOX.

SQ SEQUENCE 501 AA; 54229 MW; 45A732B009A4E5F5 CRC64;

Query Match 74.5%; Score 35; DB 1; Length 501;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2 RYIHP 7
|:|:|:|
Db 115 RYIHP 120

Fri May 24 13:12:21 2002

us-09-784-005-1.rsp

Page 10

Gencore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 24, 2002, 09:46:45 ; Search time 25.12 Seconds
(without alignments)
55.094 Million cell updates/sec

Title: US-09-784-005-1
Perfect score: 47
Sequence: 1 DRVYTHPF 8

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 segs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL.19:**
1: sp_archaea:**
2: sp_bacteria:**
3: sp_fungi:**
4: sp_human:**
5: sp_invertebrate:**
6: sp_mammal:**
7: sp_mhc:**
8: sp_organelle:**
9: sp_phage:**
10: sp_plant:**
11: sp_rodent:**
12: sp_virus:**
13: sp_vertebrate:**
14: sp_unclassified:**
15: sp_virus:**
16: sp_bacteriaph:**
17: sp_archaeap:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	47	100.0	14	5	Q10757	Q10757 Theromyzon
2	47	100.0	245	6	Q9513	Q9513 pan troglod
3	47	100.0	461	11	Q9D2V0	Q9D2V0 mus musculu
4	47	100.0	477	4	Q96FD5	Q96FD5 homo sapien
5	47	100.0	485	4	Q96F91	Q96F91 homo sapien
6	47	100.0	485	6	Q9GLP7	Q9GLP7 pan troglod
7	47	100.0	485	6	Q9GLP6	Q9GLP6 gorilla gor
8	47	100.0	485	6	Q9GLN8	Q9GLN8 pan troglod
9	47	100.0	486	6	Q9TSZ0	Q9TSZ0 callithrix
10	46	97.9	10	13	Q9PS07	Q9PS07 alligator m
11	46	87.2	293	4	Q9H444	Q9H444 homo sapien
12	40	85.1	128	16	Q9K1A7	Q9K1A7 neisseria m
13	40	85.1	132	16	Q9PG09	Q9PG09 xydella fas
14	38	80.9	171	17	Q971G2	Q971G2 sulfolobus
15	37	78.7	168	8	Q48244	Q48244 demnyus car
16	37	78.7	168	8	Q48245	Q48245 demnyus car

17	37	78.7	380	8	Q9G0M4	Q9G0M4 arapaima gl
18	36	76.6	10	13	Q9PRX8	Q9PRX8 triakis scy
19	36	76.6	124	16	Q98AV8	Q98AV8 rhizobium l
20	36	76.6	139	8	Q48241	Q48241 demnyus som
21	36	76.6	141	8	Q48240	Q48240 demnyus dis
22	36	76.6	142	8	Q48239	Q48239 demnyus dis
23	36	76.6	147	8	Q48246	Q48246 demnyus sin
24	36	76.6	161	8	Q48242	Q48242 demnyus som
25	36	76.6	167	8	Q48238	Q48238 demnyus dis
26	36	76.6	184	4	Q75406	Q75406 homo sapien
27	36	76.6	270	8	Q48257	Q48257 demnyus hir
28	36	76.6	277	10	Q80539	Q80539 arabidopsis
29	36	76.6	280	10	Q940A3	Q940A3 arabidopsis
30	36	76.6	289	10	Q9FV01	Q9FV01 arabidopsis
31	36	76.6	380	8	Q955N7	Q955N7 sphateles
32	36	76.6	449	4	Q9BVA6	Q9BVA6 homo sapien
33	36	76.6	714	5	Q9VFT7	Q9VFT7 dirosophila
34	36	76.6	728	5	Q95U29	Q95U29 demnyus tho
35	36	76.6	114	8	Q48247	Q48247 demnyus tho
36	35	74.5	141	8	Q48251	Q48251 demnyus ada
37	35	74.5	145	8	Q48252	Q48252 demnyus wel
38	35	74.5	167	8	Q48256	Q48256 demnyus cyp
39	35	74.5	168	8	Q48248	Q48248 demnyus tho
40	35	74.5	168	8	Q48249	Q48249 demnyus col
41	35	74.5	168	8	Q48250	Q48250 demnyus ada
42	35	74.5	436	11	Q9CSJ0	Q9CSJ0 demnyus mus
43	35	74.5	533	4	Q96SF7	Q96SF7 mus musculu
44	35	74.5	579	16	Q98B64	Q98B64 homo sapien
45	35	74.5	694	2	Q9EW45	Q9EW45 rhizobium l
						Q9EW45 streptomyce

ALIGNMENTS

RESULT	1	PRELIMINARY:	PRT:	14 AA.
ID	Q10757			
AC	Q10757			
DT	01-NOV-1996 (TREMBL)	01, Created		
DT	01-NOV-1996 (TREMBL)	01, Last sequence update		
DT	01-NOV-1998 (TREMBL)	08, Last annotation update		
DE	ANGIOTENSINOGEN (FRAGMENT).			
OS	Theromyzon tessulatum (leech).			
OC	Eukaryota; Metazoa; Annelida; Clitellata; Hirudindae; Hirudinea;			
OC	Rhynchobdellida; Glossiphoniidae; Theromyzon.			
OX	NCBI_TaxID=13286;			
RP	[1]			
RP	SEQUENCE:			
RX	MEDLINE=95365039; PubMed=7637887;			
RA	Laurent V., Bulet P., Salzert M.A.;			
RT	"A comparison of the leech Theromyzon tessulatum angiotensin I-like			
RT	molecule with forms of vertebrate angiotensinogens: a hormonal system			
RT	conserved in the course of evolution."			
RL	Neurosci. Lett. 190:175-178(1995).			
RN	[2]			
RP	SEQUENCE OF 1-10.			
RC	TISSUE=BRAIN;			
RX	MEDLINE=96201949; PubMed=8612806;			
RA	Laurent V., Salzert M.;			
RT	"Metabolism of angiotensins by head membranes of the leech Theromyzon			
RT	tessulatum."			
RL	FEBS Lett. 384:123-127(1996).			
CC	-1- FUNCTION: IN LEECHES THE ANGIOTENSINS ARE INVOLVED IN DIURESIS.			
KW	Glycoprotein; Serpin.			
FT	NON TER			
SO	SEQUENCE 14 AA; 1763 MW; 335109D8EEFBD7 CRC64;			

Query Match 100.0%; Score 47; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0.011; 0; Indels 0;
Matches 8; Conservative 0; Mismatches 0; Gaps 0;

QY 1 DRVYTHPF 8

Db 1 DRYIHPF 8

RESULT 2

ID 095J13 PRELIMINARY; PRT; 245 AA.

AC 095J13; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

OS ANGIOTENSINOGEN (FRAGMENT).

OC Pan troglodytes (Chimpanzee).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Pan.

NCBI_TaxID=9598;

RP SEQUENCE FROM N.A.

RC STRAIN=504, AND 505;

RA Salta Y.;

RT "Comparison of DNA and protein polymorphisms between humans and

chimpanzees."

RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB062027; BAB55856.1; -

FT NON_TER 245 245

SEQUENCE 245 AA; 26317 MW; E0092390B9803E0B CRC64;

Query Match

Best Local Similarity 100.0%; Score 47; DB 6; Length 245;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8

Db 34 DRYIHPF 41

RESULT 3

ID 09D2V0 PRELIMINARY; PRT; 461 AA.

AC 09D2V0; 01-JUN-2001 (TREMblrel. 17, Created)

DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

OS ANGIOTENSINOGEN.

OC Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

NCBI_TaxID=10990;

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=CEREBELLUM;

RA MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shingawa A., Shibata K., Yoshino M., Toh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,

RA Saito T., Okazaki Y., Gojopori T., Hono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleschmann W., Gaasterland T., Gissi C., King B., Kochwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubl F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,

RA Norioka P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyooka K., Wang K.H., Wetz C., Whitaker C., Wilming L.,

RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,

RA Hayashizaki Y.;

RA "Functional annotation of a full-length mouse cDNA collection."

RA Nature 409:685-690(2001).

DR EMBL; AK018763; BAB31393.1; -

DR MGD; MGI:87963; Agt.

DR InterPro; IPR000227; Angiotensngn.

DR InterPro; IPR000215; Serpin.

DR PRINTS; PRO0654; ANGIOTENSNGN.

DR SMART; SM00093; SERPIN.1.

SEQUENCE 461 AA; 50327 MW; 446EB081079251F CRC64;

Query Match

Best Local Similarity 100.0%; Score 47; DB 11; Length 461;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYIHPF 8

Db 30 DRYIHPF 37

RESULT 4

ID 096FD5 PRELIMINARY; PRT; 477 AA.

AC 096FD5; 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)

DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)

OS SIMILAR TO ANGIOTENSINOGEN.

OC Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

NCBI_TaxID=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=BRIN, AND GLIOBLASTOMA WITH EGFR AMPLIFICATION;

RA Strausberg R.;

RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC011519; AAH1519.1; -

SEQUENCE 485 AA; 53114 MW; 50BA5E9DC4C8E7F CRC64;

Query Match 100.0%; Score 47; DB 4; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
 |||||
 DB 34 DRYIHPF 41

RESULT 6
 O9GLP7 PRELIMINARY; PRT; 485 AA.

AC O9GLP7;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ANGIOTENSINOGEN.
 GN AGT.
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 OX NCBI_TaxID=9598;

RN [1]
 RP SEQUENCE FROM N.A.
 RA Shattuck-Bidens D., McGrail M., Stone S.;
 RT "Germline mutations in the angiotensinogen gene cause predisposition
 to type 1 diabetes mellitus."
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AF188487; AAG29056.1; -;
 DR InterPro; IPR000227; Angiotensngn.
 DR InterPro; IPR000215; Serpin.
 DR PRINTS; PRO0654; ANGIOTENSNGN.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin.
 KM SEQUENCE 485 AA; 53140 MW; 49EFB54AF31F8ADC CRC64;
 SQ

Query Match 100.0%; Score 47; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
 |||||
 DB 34 DRYIHPF 41

RESULT 7
 O9GLP6 PRELIMINARY; PRT; 485 AA.

AC O9GLP6;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ANGIOTENSINOGEN.
 GN AGT.

OS Gorilla gorilla (gorilla).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Gorilla.
 OX NCBI_TaxID=9593;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Shattuck-Bidens D., McGrail M., Stone S.;
 RT "Germline mutations in the angiotensinogen gene cause predisposition
 to type 1 diabetes mellitus."
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AF188488; AAG29057.1; -;
 DR InterPro; IPR000227; Angiotensngn.
 DR InterPro; IPR000215; Serpin.
 DR PRINTS; PRO0654; ANGIOTENSNGN.
 DR SMART; SM00093; SERPIN; 1.

DR PROSITE; PS00284; SERPIN; 1.

KW Serpin.
 SQ SEQUENCE 485 AA; 53186 MW; 53BC9235271C8255 CRC64;

Query Match 100.0%; Score 47; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
 |||||
 DB 34 DRYIHPF 41

RESULT 8
 O9GLN8 PRELIMINARY; PRT; 485 AA.

AC O9GLN8;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ANGIOTENSINOGEN.
 GN AGT.

OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
 OX NCBI_TaxID=9598;

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE-20469400; Pubmed=11013071;
 RA Dufour C., Casane D., Denton D., Wickings J., Corvol P.,
 RA Jeunemaitre X.;
 RT "Human-Chimpanzee DNA sequence variation in the four major genes of
 the renin angiotensin system."
 RT Genomics 69:14-26 (2000).
 CC -1- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
 DR EMBL; AF193461; AAG30306.1; -;
 DR EMBL; AF193458; AAG30306.1; JOINED.
 DR EMBL; AF193459; AAG30306.1; JOINED.
 DR EMBL; AF193460; AAG30306.1; JOINED.
 DR InterPro; IPR000227; Angiotensngn.
 DR InterPro; IPR000215; Serpin.
 DR PRINTS; PRO0654; ANGIOTENSNGN.
 DR SMART; SM00093; SERPIN; 1.
 DR PROSITE; PS00284; SERPIN; 1.
 KW Serpin.
 KM SEQUENCE 485 AA; 53110 MW; C14C67E49A53F05F CRC64;
 SQ

Query Match 100.0%; Score 47; DB 6; Length 485;
 Best Local Similarity 100.0%; Pred. No. 0.43;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 DRYIHPF 8
 |||||
 DB 34 DRYIHPF 41

RESULT 9
 O9TSZ0 PRELIMINARY; PRT; 486 AA.

AC O9TSZ0;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE ANGIOTENSINOGEN PRECURSOR.

GN ANGT.
 OS Callithrix jacchus (Common marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
 OX NCBI_TaxID=9483;
 RN [1]
 RP SEQUENCE FROM N.A.

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RX MEDLINE-20065005; PubMed-10598135;
RA Valdenaire O., Breu V., Giller T., Bur D., Fischli W.;
RT "Cloning and characterization of marmoset renin: comparison with human
RL renin."
CC J. Cardiovasc. Pharmacol. 34:893-897(1999).
DR EMBL: A1132343; CAB64880.1;
DR InterPro: IPR00227; Angiotensin.
DR InterPro: IPR00215; Serpin.
DR Pfam: PF00079; serpin.1.
DR PRINTS: PR00654; ANGIOTENSIN.
DR SMART: SM00093; SERPIN.1.
DR PROSITE: PS00284; SERPIN; UNKNOWN.1.
KW Serpin; signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 486 AA; 53374 MW; 5408129B2F71FB8B CRC64;

Query Match
Best Local Similarity 100.0%; Score 47; DB 6; Length 486;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVTHPF 8
DB 34 DRYVTHPF 41

RESULT 10
Q9PS07 PRELIMINARY; PRT; 10 AA.
AC Q9PS07;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE ANGIOTENSIN I, ANG I.
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylia; Alligatorinae; Alligator.
RX NCBI_Taxid=6496;
RN [1]
RP SEQUENCE.
RA MEDLINE-93307610; PubMed-8319878;
RA Takel Y., Silldorff E.P., Hasegawa Y., Watanabe T.X., Nakajima K.,
RA Stephens G.A., Sakakibara S.;
RT "New angiotensin I isolated from a reptile, Alligator
RT mississippiensis."
RL Gen. Comp. Endocrinol. 90:214-219(1993).
SQ SEQUENCE 10 AA; 1216 MW; CEE38D0761F2DB42 CRC64;

Query Match
Best Local Similarity 97.9%; Score 46; DB 13; Length 10;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVTHPF 8
DB 1 DRYVTHPF 8

RESULT 11
Q9HA44 PRELIMINARY; PRT; 295 AA.
AC Q9HA44;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DE CDNA FLJ12268 FIS, CLONE MAMMA1001627, HIGHLY SIMILAR TO HOMO SAPIENS
DE TRANSCRIPTION FACTOR TBX6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;

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RN [1]
RC SEQUENCE FROM N.A.
RC TISSUE-MAMMARY GLAND;
RA Iisogi T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,
RA Wagatsuna M., Hosoki T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
RA Takahashi M., Chiba Y., Ishida S., Murakami K., Ono Y., Takiguchi S.,
RA Yamamoto J., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
RA Niimiya K., Iwayanagi T.;
RT "NEO human cDNA sequencing project."
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK022330; BAB14014.1;
DR HSBP; P24781; 1XBR.
DR InterPro: IPR001699; T-box.
DR Pfam: PF00907; T-box.1.
DR PRINTS: PR00937; TBOX.
DR SMART: SM00425; TBOX.1.
DR PROSITE: PS01264; TBOX_2; 1.
DR PROSITE: PS0252; TBOX_3; 1.
SQ SEQUENCE 295 AA; 33197 MW; F2BD3E53E0ED21E0 CRC64;

Query Match
Best Local Similarity 87.2%; Score 41; DB 4; Length 295;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVTHPF 7
DB 170 DRYVTHPF 176

RESULT 12
Q9K1A7 PRELIMINARY; PRT; 128 AA.
AC Q9K1A7;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE HYPOTHETICAL PROTEIN NMB0260.
GN NMB0260.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
RX NCBI_Taxid=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MC58 / SEROGROUP B;
RX MEDLINE-20175755; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
RA Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
RA Smith H.O., Fraser C.M., Moxon E.R., Rappelli R., Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002382; AAF40714.1;
DR TIGR; NMB0260;
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 128 AA; 14407 MW; AAFD969E79ECFC6 CRC64;

Query Match
Best Local Similarity 85.1%; Score 40; DB 16; Length 128;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 DRYVTHPF 8
DB 23 DRYVTHPF 30

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RESULT 13
Q9PG09 PRELIMINARY; PRT; 132 AA.
ID Q9PG09:
AC Q9PG09:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOTHEtical PROTEIN XE0493.
GN XE0493.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xylella.
OC NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347;
RA Simpson A.J.G., Rehnach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorri H.,
RA Facinani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hobeisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A.Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmeri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A.Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Silveira W.J., de Souza A.A.,
RA de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tsuchioka M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Zeldanis J., Zetubai J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
DR EMBL; AF003898; AAF83303.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 132 AA; 14458 MW; E69EF1ECD9915E1F CRC64;

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Query Match 85.1%; Score 40; DB 16; Length 132;
Best Local Similarity 62.5%; Pred. No. 2.6;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYVTHP 8
|:|||||
Db 91 DRIHVHP 98

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RESULT 14
Q971G2 PRELIMINARY; PRT; 171 AA.
AC Q971G2:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE HYPOTHEtical PROTEIN ST1391.
GN ST1391.
OS Sulfolobus tokodaii.
OC Archaea; Crenarchaeota; Sulfolobales; Sulfolobaceae; Sulfolobus.
OC NCBI_TaxID=111955;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=JCM 10545 / 7;
RX PubMed=11572479;
RA Kawarabayashi Y., Hino Y., Horikawa H., Jinno K., Takahashi M.,
RA Sekine M., Baba S.-I., Anka A., Kosugi H., Hosoyama A., Fukui S.,
RA Nagai Y., Nishijima K., Otsuka R., Nakazawa H., Takamiya M., Kato Y.,
RA Yoshizawa T., Tanaka T., Kudoh Y., Yamazaki J., Kushiida N., Oguchi A.,
RA Aoki K.-I., Masuda S., Yanagii M., Nishimura M., Yamagishi A.,
RA Oshima T., Kikuchi H.;
RT "Complete genome sequence of an aerobic thermophilic
RT Crenarchaeon, Sulfolobus tokodaii strain7.";
RL DNA Res. 8:123-140(2001).
DR EMBL; AP000986; BAB66458.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 171 AA; 18700 MW; 897F397EAD34EF0A CRC64;

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Query Match 80.9%; Score 38; DB 17; Length 171;
Best Local Similarity 78.7%; Pred. No. 8.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 DRYVTHP 7
|:|||||
Db 16 DRYVTHP 22

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RESULT 15
Q48244 PRELIMINARY; PRT; 168 AA.
ID Q48244:
AC Q48244:
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE CYTOCHROME B (FRAGMENT).
GN CYTB.
OS Dennyus carljonesi fosteri.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Plekoyota; Neoptera; Paraneoptera; Phlebotomera; Amblycera;
OC Menoponidae; Dennyus.
OX NCBI_TaxID=60502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=541;
RX MEDLINE=98224083; PubMed=9562986;
RA Page R.D., Lee P.L., Becher S.A., Griffiths R., Clayton D.H.;
RT "A different tempo of mitochondrial DNA evolution in birds and their
RT parasitic lice.";
RL Mol. Phylogenet. Evol. 9:276-293(1998).
CC -I- FUNCTION: COMPONENT OF THE UBICUINOL-CYTOCHROME C REDUCTASE
CC COMPLEX (COMPLEX III OR CYTOCHROME B-C1 COMPLEX), WHICH IS A
CC RESPIRATORY CHAIN THAT GENERATES AN ELECTROCHEMICAL POTENTIAL
CC COUPLED TO ATP SYNTHESIS (BY SIMILARITY).
CC -I- COFACTOR: TWO HEME GROUPS (B562 AND B566) WHICH ARE NOT COVALENTLY
CC BOUND TO THE PROTEIN (BY SIMILARITY).
CC -I- SUBUNIT: THE MAIN SUBUNITS OF COMPLEX B-C1 ARE: CYTOCHROME B,
CC CYTOCHROME C1 AND THE RIESKE PROTEIN (BY SIMILARITY).
CC -I- SIMILARITY: BELONGS TO THE CYTOCHROME B FAMILY.
DR EMBL; U96421; AAB91357.1; -
DR InterPro: IPR000179; Cyt.b.b6.
DR Pfam: PF00033; cytochrome_b_n; 1.
KW Electron transport; Heme; Mitochondrion; Respiratory chain;
KW Transmembrane.
FT NON_TER 1
FT NON_TER 168
SQ SEQUENCE 168 AA; 19548 MW; 18F63948414BD21A CRC64;

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Query Match 78.7%; Score 37; DB 8; Length 168;
Best Local Similarity 62.5%; Pred. No. 13;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DRYVTHP 8

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Db 113 DKVYFHPY 120

Search completed: May 24, 2002, 09:50:22
Job time: 217 sec